

SEQUENCE LISTING

<110> Lanahan, Mike

<120> Self-processing Plants and Plant Parts

<130> 109846.317

<140> US 60/315,281

<141> 2001-08-27

<160> 112

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 436

<212> FRT

<213> Artificial Sequence

<220>

<223> synthetic

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Glu	Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr		
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Ile	Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala	Trp	Val		
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Val	Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr		
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225					230				235						240		
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His Asp Thr Asp Ile Ile Trp Asn	Lys Tyr Pro Ala Tyr Ala Phe Ile				
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Leu Thr Tyr Glu Gly Gln Pro Thr	Ile Phe Tyr Arg Asp Tyr Glu Glu				
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Trp Leu Asn Lys Asp Lys Leu Lys	Asn Leu Ile Trp Ile His Asp Asn				
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Leu Ala Gly Gly Ser Thr Ser Ile	Val Tyr Tyr Asp Ser Asp Glu Met				
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Ile Phe Val Arg Asn Gly Tyr Gly	Ser Lys Pro Gly Leu Ile Thr Tyr				
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Ile Asn Leu Gly Ser Ser Lys Val	Gly Arg Trp Val Tyr Val Pro Lys				
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Phe Ala Gly Ala Cys Ile His Glu	Tyr Thr Gly Asn Leu Gly Gly Trp				
385	390	395			400
Val Asp Lys Tyr Val Tyr Ser Ser	Gly Trp Val Tyr Leu Glu Ala Pro				
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<211> 1308

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 2

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<210> 3

<211> 800
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 3
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 35 40 45
 Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala Glu Val Trp
 50 55 60
 Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro Asp Thr Ser
 65 70 75 80
 Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val Ile Glu Ala
 85 90 95
 Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Glu Leu Phe Lys Val
 100 105 110
 Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu Lys Ala Asp
 115 120 125
 Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val Leu Ser Glu
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 Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu Ile Ile Glu
 145 150 155 160
 Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu Asp Asp Tyr
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 Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu Lys Thr Ile
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 Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val Leu Leu Phe
 195 200 205
 Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn Met Glu Tyr
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 Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp Leu Asp Gly
 225 230 235 240
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 245 250 255
 Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln Glu Ser Ala
 260 265 270
 Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu Asn Asp Arg
 275 280 285
 Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr Glu Ile His
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 Ile Ala Asp Ile Thr Gly Leu Glu Asn Ser Gly Val Lys Asn Lys Gly
 305 310 315 320
 Leu Tyr Leu Gly Leu Thr Glu Glu Asn Thr Lys Gly Pro Gly Gly Val
 325 330 335
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 Ile Leu Pro Phe Phe Asp Phe Tyr Thr Gly Asp Glu Leu Asp Lys Asp
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 Phe Glu Lys Tyr Tyr Asn Trp Gly Tyr Asp Pro Tyr Leu Phe Met Val
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 Pro Glu Gly Arg Tyr Ser Thr Asp Pro Lys Asn Pro His Thr Arg Ile
 385 390 395 400

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      435      440      445
Thr Gly Ala Tyr Leu Asn Glu Ser Gly Cys Gly Asn Val Ile Ala Ser
      450      455      460
Glu Arg Pro Met Met Arg Lys Phe Ile Val Asp Thr Val Thr Tyr Trp
465      470      475      480
Val Lys Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Gln Met Gly Leu
      485      490      495
Ile Asp Lys Lys Thr Met Leu Glu Val Glu Arg Ala Leu His Lys Ile
      500      505      510
Asp Pro Thr Ile Ile Leu Tyr Gly Glu Pro Trp Gly Gly Trp Gly Ala
      515      520      525
Pro Ile Arg Phe Gly Lys Ser Asp Val Ala Gly Thr His Val Ala Ala
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Phe Asn Asp Glu Phe Arg Asp Ala Ile Arg Gly Ser Val Phe Asn Pro
545      550      555      560
Ser Val Lys Gly Phe Val Met Gly Gly Tyr Gly Lys Glu Thr Lys Ile
      565      570      575
Lys Arg Gly Val Val Gly Ser Ile Asn Tyr Asp Gly Lys Leu Ile Lys
      580      585      590
Ser Phe Ala Leu Asp Pro Glu Glu Thr Ile Asn Tyr Ala Ala Cys His
      595      600      605
Asp Asn His Thr Leu Trp Asp Lys Asn Tyr Leu Ala Ala Lys Ala Asp
      610      615      620
Lys Lys Lys Glu Trp Thr Glu Glu Glu Leu Lys Asn Ala Gln Lys Leu
625      630      635      640
Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe Leu His Gly
      645      650      655
Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn Ser Tyr Asn
      660      665      670
Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys Leu Gln Phe
      675      680      685
Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu Arg Lys Glu
      690      695      700
His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys Lys His Leu
705      710      715      720
Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met Leu Lys Asp
      725      730      735
His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile Tyr Asn Gly
      740      745      750
Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys Trp Asn Val
      755      760      765
Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu Thr Val Glu
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<210> 4
 <211> 2400
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 4

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<211> 693

<212> PRT

<213> *Sulfolobus solfataricus*

<400> 5

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Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile Val Gln Gln
 35           40           45
Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys Glu His Ile

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Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys Asp Gly Val		95
	100	105
Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile Phe Asp Val		110
	115	120
Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro Glu Asp Ser		125
	130	135
Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp Val Leu Glu		140
145	150	155
Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro Met Trp Ala		160
	165	170
Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln Asp Lys Val		175
	180	185
Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg Val Ala Gly		190
	195	200
Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu Phe Thr Trp		205
210	215	220
His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp Glu Leu His		225
225	230	235
Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly Ile Arg Val		240
	245	250
Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys Phe Cys Glu		255
	260	265
Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro Gly Thr Thr		270
	275	280
Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp Trp Ala Gly		285
290	295	300
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305	310	315
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Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Asp Arg Leu Val Thr Thr		335
	340	345
Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg Val Lys His		350
	355	360
Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met Ala Thr Phe		365
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Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile Leu Ser Arg		385
385	390	395
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Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp Ile Gly Gly		430
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Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met Asp Leu Leu		445
	450	455
Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr Arg Ser His		460
465	470	475
Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu Pro Asp Tyr		480
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<211> 1818

<212> DNA

<213> Artificial Sequence

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<223> synthetic

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<210> 8

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 8
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Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg Thr
35 40 45
Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg Gly
50 55 60
Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Met Asn Val
65 70 75 80
Val Phe Val Gly Ala Glu Met Ala Pro Trp Ser Lys Thr Gly Gly Leu
85 90 95
Gly Asp Val Leu Gly Gly Leu Pro Pro Ala Met Ala Ala Asn Gly His
100 105 110
Arg Val Met Val Val Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp
115 120 125
Asp Thr Ser Val Val Ser Glu Ile Lys Met Gly Asp Gly Tyr Glu Thr
130 135 140
Val Arg Phe Phe His Cys Tyr Lys Arg Gly Val Asp Arg Val Phe Val
145 150 155 160
Asp His Pro Leu Phe Leu Glu Arg Val Trp Gly Lys Thr Glu Glu Lys
165 170 175
Ile Tyr Gly Pro Val Ala Gly Thr Asp Tyr Arg Asp Asn Gln Leu Arg
180 185 190
Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu Ala Pro Arg Ile Leu Ser
195 200 205
Leu Asn Asn Asn Pro Tyr Phe Ser Gly Pro Tyr Gly Glu Asp Val Val
210 215 220
Phe Val Cys Asn Asp Trp His Thr Gly Pro Leu Ser Cys Tyr Leu Lys
225 230 235 240
Ser Asn Tyr Gln Ser His Gly Ile Tyr Arg Asp Ala Lys Thr Ala Phe
245 250 255
Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe Ser Asp Tyr
260 265 270
Pro Glu Leu Asn Leu Pro Glu Arg Phe Lys Ser Ser Phe Asp Phe Ile
275 280 285
Asp Gly Tyr Glu Lys Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys
290 295 300
Ala Gly Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr
305 310 315 320
Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn
325 330 335
Ile Met Arg Leu Thr Gly Ile Thr Gly Ile Val Asn Gly Met Asp Val
340 345 350
Ser Glu Trp Asp Pro Ser Arg Asp Lys Tyr Ile Ala Val Lys Tyr Asp
355 360 365
Val Ser Thr Ala Val Glu Ala Lys Ala Leu Asn Lys Glu Ala Leu Gln
370 375 380
Ala Glu Val Gly Leu Pro Val Asp Arg Asn Ile Pro Leu Val Ala Phe
385 390 395 400
Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro Asp Val Met Ala Ala Ala
405 410 415
Ile Pro Gln Leu Met Glu Met Val Glu Asp Val Gln Ile Val Leu Leu
420 425 430
Gly Thr Gly Lys Lys Lys Phe Glu Arg Met Leu Met Ser Ala Glu Glu
435 440 445
Lys Phe Pro Gly Lys Val Arg Ala Val Val Lys Phe Asn Ala Ala Leu

450	Ala	His	His	Ile	Met	Ala	Gly	Ala	Asp	Val	Leu	Ala	Val	Thr	Ser	Arg
465	Phe	Glu	Pro	Cys	Gly	Leu	Ile	Gln	Leu	Gln	Gly	Met	Arg	Tyr	Gly	Thr
	Pro	Cys	Ala	Cys	Ala	Ser	Thr	Gly	Gly	Leu	Val	Asp	Thr	Ile	Ile	Glu
	Gly	Lys	Thr	Gly	Phe	His	Met	Gly	Arg	Leu	Ser	Val	Asp	Cys	Asn	Val
	Val	Glu	Pro	Ala	Asp	Val	Lys	Lys	Val	Ala	Thr	Thr	Leu	Gln	Arg	Ala
	Ile	Lys	Val	Val	Gly	Thr	Pro	Ala	Tyr	Glu	Glu	Met	Val	Arg	Asn	Cys
	Met	Ile	Gln	Asp	Leu	Ser	Trp	Lys	Gly	Pro	Ala	Lys	Asn	Trp	Glu	Asn
	Val	Leu	Leu	Ser	Leu	Gly	Val	Ala	Gly	Gly	Glu	Pro	Gly	Val	Glu	Gly
	Glu	Glu	Ile	Ala	Pro	Leu	Ala	Lys	Glu	Asn	Val	Ala	Ala	Pro		

<210> 9
 <211> 2223
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 9

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gccggcatct	ccgcgatctg	gataccgcca	gcttccaagg	gcatgtccgg	gggctactcg	180
atgggctacg	acccgtacga	ctacttcgac	ctcggcgagt	actaccagaa	gggcacggtg	240
gagacgcgct	tcgggtccaa	gcaggagctc	atcaacatga	tcaacacggc	gcacgcctac	300
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gtgggcgagt	actgggacac	caacgtcgac	gcgctgctca	actgggccta	ctcctccggc	720
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tcgaagcccg	gcctgatcac	gtacatcaac	ctgggctcct	ccaagggtgg	ccgctgggtg	1140
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gtggacaagt	acgtgtactc	ctccggctgg	gtctacctgg	aggccccggc	ctacgacccc	1260
gccaaacggc	agtacggcta	ctccgtgtgg	tcctactgcg	gcgtcggcac	atcgattgct	1320
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<210> 10

<211> 741

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 10

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          20          25          30
Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
          35          40          45
Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
          50          55          60
Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
65          70          75          80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
          85          90          95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
          100          105          110
Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
          115          120          125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
          130          135          140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
          145          150          155          160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
          165          170          175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
          180          185          190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
          195          200          205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
          210          215          220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
          225          230          235          240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
          245          250          255
Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly
          260          265          270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
          275          280          285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
          290          295          300

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Leu	Thr	Tyr	Glu	Gly	Gln	Pro	Thr	Ile	Phe	Tyr	Arg	Asp	Tyr	Glu	Glu
305					310				315					320	
Trp	Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His	Asp	Asn
				325					330					335	
Leu	Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Tyr	Asp	Ser	Asp	Glu	Met
			340					345					350		
Ile	Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile	Thr	Tyr
		355					360					365			
Ile	Asn	Leu	Gly	Ser	Ser	Lys	Val	Gly	Arg	Trp	Val	Tyr	Val	Pro	Lys
	370					375					380				
Phe	Ala	Gly	Ala	Cys	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly	Gly	Trp
385					390					395					400
Val	Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu	Ala	Pro
				405					410					415	
Ala	Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp	Ser	Tyr
			420					425					430		
Cys	Gly	Val	Gly	Thr	Ser	Ile	Ala	Gly	Ile	Leu	Glu	Ala	Asp	Arg	Val
		435					440					445			
Leu	Thr	Val	Ser	Pro	Tyr	Tyr	Ala	Glu	Glu	Leu	Ile	Ser	Gly	Ile	Ala
	450				455						460				
Arg	Gly	Cys	Glu	Leu	Asp	Asn	Ile	Met	Arg	Leu	Thr	Gly	Ile	Thr	Gly
465					470				475						480
Ile	Val	Asn	Gly	Met	Asp	Val	Ser	Glu	Trp	Asp	Pro	Ser	Arg	Asp	Lys
			485						490					495	
Tyr	Ile	Ala	Val	Lys	Tyr	Asp	Val	Ser	Thr	Ala	Val	Glu	Ala	Lys	Ala
			500					505					510		
Leu	Asn	Lys	Glu	Ala	Leu	Gln	Ala	Glu	Val	Gly	Leu	Pro	Val	Asp	Arg
		515					520					525			
Asn	Ile	Pro	Leu	Val	Ala	Phe	Ile	Gly	Arg	Leu	Glu	Glu	Gln	Lys	Gly
	530					535					540				
Pro	Asp	Val	Met	Ala	Ala	Ala	Ile	Pro	Gln	Leu	Met	Glu	Met	Val	Glu
545					550					555					560
Asp	Val	Gln	Ile	Val	Leu	Leu	Gly	Thr	Gly	Lys	Lys	Lys	Phe	Glu	Arg
				565					570					575	
Met	Leu	Met	Ser	Ala	Glu	Glu	Lys	Phe	Pro	Gly	Lys	Val	Arg	Ala	Val
			580					585					590		
Val	Lys	Phe	Asn	Ala	Ala	Leu	Ala	His	His	Ile	Met	Ala	Gly	Ala	Asp
		595					600					605			
Val	Leu	Ala	Val	Thr	Ser	Arg	Phe	Glu	Pro	Cys	Gly	Leu	Ile	Gln	Leu
	610					615					620				
Gln	Gly	Met	Arg	Tyr	Gly	Thr	Pro	Cys	Ala	Cys	Ala	Ser	Thr	Gly	Gly
625					630				635						640
Leu	Val	Asp	Thr	Ile	Ile	Glu	Gly	Lys	Thr	Gly	Phe	His	Met	Gly	Arg
				645					650					655	
Leu	Ser	Val	Asp	Cys	Asn	Val	Val	Glu	Pro	Ala	Asp	Val	Lys	Lys	Val
			660					665					670		
Ala	Thr	Thr	Leu	Gln	Arg	Ala	Ile	Lys	Val	Val	Gly	Thr	Pro	Ala	Tyr
		675					680					685			
Glu	Glu	Met	Val	Arg	Asn	Cys	Met	Ile	Gln	Asp	Leu	Ser	Trp	Lys	Gly
	690					695					700				
Pro	Ala	Lys	Asn	Trp	Glu	Asn	Val	Leu	Leu	Ser	Leu	Gly	Val	Ala	Gly
705					710					715					720
Gly	Glu	Pro	Gly	Val	Glu	Gly	Glu	Glu	Ile	Ala	Pro	Leu	Ala	Lys	Glu
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Asn	Val	Ala	Ala	Pro											
			740												

<210> 11
 <211> 1515
 <212> DNA
 <213> Zea mays

<400> 11
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 cagctcagaa aaaagttatc tatgaaaggt ttcattgtga ccgtgggaaa tgagaaatgt 180
 tgccaactca aacaccttca atatgttggt tgcaggcaaa ctcttctgga agaaaggtgt 240
 ctaaaactat gaacgggtta cagaaaggta taaaccacgg ctgtgcattt tggaagtatc 300
 atctatagat gtctgttgag gggaaagccg tacgccaacg ttatttactc agaaacagct 360
 tcaacacaca gttgtctgct ttatgatggc atctccaccc aggcacccac catcacctat 420
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 aacatgcata ggcataatcaa tatgtctatt tattaatttg ctacgagatc atcttcctac 540
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 ccaatgcate ttcattaaat gtgaatttca gaaaggaagt aggaacctat gagagtattt 660
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 cactaatgat ggttgggttg atgagttctg cgattacttg caagaaatgt gaacctttgt 780
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 ttcagttttg tcataagatg tcatattaaa gggcaaacat atattcaatg ttcaattcat 1440
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 tagtagttgg aggag 1515

<210> 12
 <211> 673
 <212> DNA
 <213> Zea mays

<400> 12
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 aattgcacgt caagggtatt gggtaagaaa caatcaaaaa aatcctctct gtgtgcaaag 180
 aaacacggtg agtcatgccg agatcatact catctgatat acatgcttac agctcacaag 240
 acattacaaa caactcatat tgcattacaa agatcgtttc atgaaaaata aaataggccg 300
 gacaggacaa aaatccttga cgtgtaaaagt aaatttacaa caaaaaaaaa gccatatgtc 360
 aagctaaatc taattcgttt tacgtagatc aacaacctgt agaaggcaac aaaactgagc 420
 cagcgagaag tacagaatga ttccagatga accatcgacg tgctacgtaa agagagtgac 480
 gagtcatata catttggcaa gaaacatga agctgcctac agccgtctcg gtggcataag 540
 aacacaagaa attgtgttaa ttaatcaaa ctataaataa cgctcgcatg cctgtgcact 600
 tctccatcac caccactggg tcttcagacc attagcttta tctactccag agcgacagaag 660
 aaccgatcg aca 673

<210> 13
 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 13

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      20      25      30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
      35      40      45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
      50      55      60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65      70      75      80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
      85      90      95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
      100      105      110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
      115      120      125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
      130      135      140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145      150      155      160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
      165      170      175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
      180      185      190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
      195      200      205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
210      215      220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225      230      235      240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
      245      250      255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
      260      265      270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
      275      280      285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
290      295      300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305      310      315      320
Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
      325      330      335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
      340      345      350
Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
      355      360      365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
      370      375      380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
385      390      395      400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
      405      410      415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
      420      425      430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp

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435
Ser Tyr Cys Gly Val Gly
450

440

445

<210> 14
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 14

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		20					25						30		
Gln	Ala	Phe	Tyr	Trp	Asp	Val	Pro	Ser	Gly	Gly	Ile	Trp	Trp	Asp	Thr
		35					40					45			
Ile	Arg	Gln	Lys	Ile	Pro	Glu	Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile
	50					55					60				
Trp	Ile	Pro	Pro	Ala	Ser	Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly
65				70					75					80	
Tyr	Asp	Pro	Tyr	Asp	Tyr	Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly
			85					90					95		
Thr	Val	Glu	Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile
			100					105					110		
Asn	Thr	Ala	His	Ala	Tyr	Gly	Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile
		115					120					125			
Asn	His	Arg	Ala	Gly	Gly	Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Gly	Asp
	130					135					140				
Tyr	Thr	Trp	Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala
145				150					155					160	
Asn	Tyr	Leu	Asp	Phe	His	Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly
			165					170					175		
Thr	Phe	Gly	Gly	Tyr	Pro	Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln
		180					185						190		
Tyr	Trp	Leu	Trp	Ala	Ser	Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser
	195					200						205			
Ile	Gly	Ile	Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala
	210					215					220				
Trp	Val	Val	Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly
225				230						235				240	
Glu	Tyr	Trp	Asp	Thr	Asn	Val	Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Ser
			245					250					255		
Ser	Gly	Ala	Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala
		260					265						270		
Ala	Phe	Asp	Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn
		275					280					285			
Gly	Gly	Thr	Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val
	290					295					300				
Ala	Asn	His	Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala
305				310					315					320	
Phe	Ile	Leu	Thr	Tyr	Glu	Gly	Gln	Pro	Thr	Ile	Phe	Tyr	Arg	Asp	Tyr
			325					330					335		
Glu	Glu	Trp	Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His
		340					345					350			

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Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
      355      360      365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
      370      375      380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
385      390      395      400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
      405      410      415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
      420      425      430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
      435      440      445
Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
      450      455      460

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<210> 15
<211> 518
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic

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<400> 15
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 1      5      10      15
Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
      20      25      30
Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
      35      40      45
Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
      50      55      60
Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
65      70      75      80
Ala Lys Tyr Leu Glu Leu Glu Gly Gly Val Ile Met Gln Ala Phe
      85      90      95
Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
      100      105      110
Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro
      115      120      125
Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro
      130      135      140
Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu
145      150      155      160
Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala
      165      170      175
His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg
      180      185      190
Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp
      195      200      205
Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
      210      215      220
Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly
225      230      235      240
Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu
      245      250      255
Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile

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<400> 16																
Met	Leu	Ala	Ala	Leu	Ala	Thr	Ser	Gln	Leu	Val	Ala	Thr	Arg	Ala	Gly	
1				5					10					15		
Leu	Gly	Val	Pro	Asp	Ala	Ser	Thr	Phe	Arg	Arg	Gly	Ala	Ala	Gln	Gly	
			20					25					30			
Leu	Arg	Gly	Ala	Arg	Ala	Ser	Ala	Ala	Ala	Asp	Thr	Leu	Ser	Met	Arg	
		35					40					45				
Thr	Ser	Ala	Arg	Ala	Ala	Pro	Arg	His	Gln	His	Gln	Gln	Ala	Arg	Arg	
	50					55					60					
Gly	Ala	Arg	Phe	Pro	Ser	Leu	Val	Val	Cys	Ala	Ser	Ala	Gly	Ala	Met	
65					70					75					80	
Ala	Lys	Tyr	Leu	Glu	Leu	Glu	Glu	Gly	Gly	Val	Ile	Met	Gln	Ala	Phe	
				85					90					95		
Tyr	Trp	Asp	Val	Pro	Ser	Gly	Gly	Ile	Trp	Trp	Asp	Thr	Ile	Arg	Gln	
			100					105					110			

Lys	Ile	Pro	Glu	Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Pro	115	120	125
Pro	Ala	Ser	Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp	Pro	130	135	140
Tyr	Asp	Tyr	Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val	Glu	145	150	155
Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr	Ala	165	170	175
His	Ala	Tyr	Gly	Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	180	185	190
Ala	Gly	Gly	Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Gly	Asp	Tyr	Thr	Trp	195	200	205
Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr	Leu	210	215	220
Asp	Phe	His	Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly	Thr	Phe	Gly	225	230	235
Gly	Tyr	Pro	Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln	Tyr	Trp	Leu	245	250	255
Trp	Ala	Ser	Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly	Ile	260	265	270
Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala	Trp	Val	Val	275	280	285
Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr	Trp	290	295	300
Asp	Thr	Asn	Val	Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Gly	Ala	305	310	315
Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala	Ala	Phe	Asp	325	330	335
Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn	Gly	Gly	Thr	340	345	350
Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val	Ala	Asn	His	355	360	365
Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	Phe	Ile	Leu	370	375	380
Thr	Tyr	Glu	Gly	Gln	Pro	Thr	Ile	Phe	Tyr	Arg	Asp	Tyr	Glu	Glu	Trp	385	390	395
Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His	Asp	Asn	Leu	405	410	415
Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Tyr	Asp	Ser	Asp	Glu	Met	Ile	420	425	430
Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile	Thr	Tyr	Ile	435	440	445
Asn	Leu	Gly	Ser	Ser	Lys	Val	Gly	Arg	Trp	Val	Tyr	Val	Pro	Lys	Phe	450	455	460
Ala	Gly	Ala	Cys	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly	Gly	Trp	Val	465	470	475
Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu	Ala	Pro	Ala	485	490	495
Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp	Ser	Tyr	Cys	500	505	510
Gly	Val	Gly	Thr	Ser	Ile	Ala	Gly	Ile	Leu	Glu	Ala	Asp	Arg	Val	Leu	515	520	525
Thr	Val	Ser	Pro	Tyr	Tyr	Ala	Glu	Glu	Leu	Ile	Ser	Gly	Ile	Ala	Arg	530	535	540
Gly	Cys	Glu	Leu	Asp	Asn	Ile	Met	Arg	Leu	Thr	Gly	Ile	Thr	Gly	Ile	545	550	555
Val	Asn	Gly	Met	Asp	Val	Ser	Glu	Trp	Asp	Pro	Ser	Arg	Asp	Lys	Tyr	565	570	575


```

Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala Leu
      580      585      590
Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg Asn
      595      600      605
Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro
      610      615      620
Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu Asp
      625      630      635      640
Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Arg Met
      645      650      655
Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val Val
      660      665      670
Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp Val
      675      680      685
Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu Gln
      690      695      700
Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu
      705      710      715      720
Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu
      725      730      735
Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val Ala
      740      745      750
Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu
      755      760      765
Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly Pro
      770      775      780
Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly Gly
      785      790      795      800
Glu Pro Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu Asn
      805      810      815
Val Ala Ala Pro
      820

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<210> 17
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 17
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser

<210> 18
 <211> 444
 <212> PRT
 <213> Thermotoga maritima

<400> 18
 Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Ile Gln Phe Glu Gly Lys
 1 5 10 15
 Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val

<210>	19
<211>	1335
<212>	DNA

<213> *Thermotoga maritima*

<400> 19

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cacctcaagt tctccgtggc cttctggcac accttcgtga acgagggccg cgaccggttc 180
ggcgaccgga ccgccgagcg cccgtggaac cgcttctccg acccgatgga caaggccttc 240
gcccgcctgg acgcccctct cgagttctgc gagaagctca acatcgagta cttctgcttc 300
cacgaccgcg acatcgcccc ggagggcaag acctcccgcg agaccaacaa gatcctcgac 360
aaggtggtgg agcgcatcaa ggagcgcatg aaggactcca acgtgaagct cctctggggc 420
accgccaacc tcttctccca cccgcgctac atgcacggcg ccgccaccac ctgctccgcc 480
gacgtgttcg cctacgcccg cgcccaggtg aagaaggccc tggagatcac caaggagctg 540
ggcgcggaag gctacgtgtt ctggggcgcg cgcgagggtt acgagaccct cctcaacacc 600
gacctcgggc tggagctgga gaacctcgcc cgcttctctc gcatggccgt ggagtacgcc 660
aagaagatcg gcttcaccgg ccagttcctc atcgagccga agccgaagga gccgaccaag 720
caccagtacg acctcgacgt ggccaccgcc tacgccttcc tcaagaacca cggcctcgac 780
gagtaactta agttcaacat cgagggcaac cagccaccac tcgcccggca cactttccag 840
cacgagctgc gcatggcccg catcctcggc aagctcggtt ccacgacgc caaccagggc 900
gacctcctcc tcggctggga caccgaccag ttcccgaaca acatctacga caccaccttc 960
gccatgtacg aggtgatcaa ggccggcgcg ttaccaagg gcggcctcaa cttcgacgcc 1020
aaggtgcgcc gcgctccta caaggtggag gacctcttca tcggccacat cgccggcatg 1080
gacaccttcg cctcggctt caagatcgcc tacaagctcg ccaaggacgg cgtgttcgac 1140
aagttcatcg aggagaagta ccgctccttc aaggagggca tcggcaagga gatcgtggag 1200
ggcaagaccg acctcgagaa gctggaggag tacatcatcg acaaggagga catcgagctg 1260
ccgtccggca agcaggagta cctggagtcc ctctcaact cctacatcgt gaagaccatc 1320
gccgagctgc gctga

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<210> 20

<211> 444

<212> PRT

<213> *Thermotoga neapolitana*

<400> 20

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Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe Glu Gly Lys
1      5      10      15
Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro Glu Glu Ile
20      25      30
Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe
35      40      45
Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr
50      55      60
Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp Lys Ala Phe
65      70      75      80
Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu
85      90      95
Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu
100     105     110
Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu
115     120     125
Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu
130     135     140
Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala
145     150     155     160
Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile
165     170     175
Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu
180     185     190
Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu Leu Glu Asn

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195	200	205
Leu Ala Arg Phe Leu Arg Met	Ala Val Asp Tyr	Ala Lys Arg Ile Gly
210	215	220
Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro	Lys Glu Pro Thr Lys	
225	230	235
His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr	Ala Phe Leu Lys Ser	
245	250	255
His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile	Glu Ala Asn His Ala	
260	265	270
Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg	Met Ala Arg Ile	
275	280	285
Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln	Gly Asp Leu Leu Leu	
290	295	300
Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val	Tyr Asp Thr Thr Leu	
305	310	315
Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe	Thr Lys Gly Gly Leu	
325	330	335
Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr	Lys Val Glu Asp Leu	
340	345	350
Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe	Ala Leu Gly Phe Lys	
355	360	365
Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu	Asp Lys Phe Ile Glu	
370	375	380
Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly	Arg Asp Ile Val Glu	
385	390	395
Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr	Ile Ile Asp Lys Glu	
405	410	415
Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr	Leu Glu Ser Leu Ile	
420	425	430
Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg		
435	440	

<210> 21

<211> 1335

<212> DNA

<213> Thermotoga neapolitana

<400> 21

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cacctcaagt tctccgtggc cttctggcac accttcgtga acgagggccg cgacccgttc 180
ggcgacccga ccgcccagcc cccgtggaac cgctacaccg acccgatgga caaggccttc 240
gcccgcgtgg acgcccctct cgagttctgc gagaagctca acatcgagta cttctgcttc 300
cacgaccgcg acatcgcccc ggagggcaag accctccgcg agaccaacaa gatcctcgac 360
aaggtggtgg agcgcaccaa ggagcgcgat aaggactcca acgtgaagct cctctggggc 420
accgccsacc tcttctccca cccgcgctac atgcacggcg ccgccaccac ctgctccgcc 480
gacgtgttcg cctacgcccg cgcccagggt aagaaggccc tggagatcac caaggagctg 540
ggcggcgagg gctacgtgtt ctggggcggc cgcgagggt acgagaccct cctcaacacc 600
gacctcggtt tcgagctgga gaacctcgcc cgcttcctcc gcatggccgt ggactacgcc 660
aagcgcacat gcttcaccgg ccagttcctc atcgagccga agccgaagga gccgaccaag 720
caccagtacg acttcgacgt ggccaccgcc tacgccttc tcaagtccca cggcctcgac 780
gagtacttca agttcaacat cgaggccaac cagccacccc tcgccggcca caccttccag 840
cacgagctgc gcatggcccc catcctcggc aagctcggct ccacgcacgc caaccagggc 900
gacctcctcc tcggctggga caccgaccag ttcccgaaca acgtgtacga caccaccctc 960
gccatgtacg aggtgatcaa ggccggcggc ttaccaaggg gcggcctcaa cttcgacgcc 1020
aaggtgcgcc gcgcctccta caaggtggag gacctcttca tcggccacat cgccggcatg 1080
gacaccttcg ccctcggttt caaggtggcc tacaagctcg tgaaggacgg cgtgctcgac 1140

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aagttcatcg aggagaagta ccgctccttc cgcgagggca tcggccgcga catcgtggag 1200
 ggcaagggtgg acttcgagaa gctggaggag tacatcatcg acaaggagac catcgagctg 1260
 ccgtccggca agcaggagta cctggagtcc ctcacaaact cctacatcgt gaagaccatc 1320
 ctggagctgc gctga 1335

<210> 22
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 22
 agcgaattca tggcggctct ggccacgt 28

<210> 23
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 23
 agctaagctt cagggcgcgg ccacgttct 29

<210> 24
 <211> 325
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 24
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 Ala Thr Ser Ala Gly His Trp Tyr Lys His Gln Arg Ala Tyr Gln Phe
 20 25 30
 Thr Gly Glu Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met
 35 40 45
 Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
 50 55 60
 Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
 65 70 75 80
 Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
 85 90 95
 Asp Thr Ser Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val
 100 105 110
 Ile Glu Ala Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu
 115 120 125
 Phe Lys Val Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu
 130 135 140
 Lys Ala Asp Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val
 145 150 155 160
 Leu Ser Glu Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu
 165 170 175

Ile	Ile	Glu	Gly	Tyr	Lys	Pro	Ala	Arg	Val	Ile	Met	Met	Glu	Ile	Leu
			180					185					190		
Asp	Asp	Tyr	Tyr	Tyr	Asp	Gly	Glu	Leu	Gly	Ala	Val	Tyr	Ser	Pro	Glu
		195					200					205			
Lys	Thr	Ile	Phe	Arg	Val	Trp	Ser	Pro	Val	Ser	Lys	Trp	Val	Lys	Val
	210					215					220				
Leu	Leu	Phe	Lys	Asn	Gly	Glu	Asp	Thr	Glu	Pro	Tyr	Gln	Val	Val	Asn
225					230					235					240
Met	Glu	Tyr	Lys	Gly	Asn	Gly	Val	Trp	Glu	Ala	Val	Val	Glu	Gly	Asp
				245					250					255	
Leu	Asp	Gly	Val	Phe	Tyr	Leu	Tyr	Gln	Leu	Glu	Asn	Tyr	Gly	Lys	Ile
			260					265					270		
Arg	Thr	Thr	Val	Asp	Pro	Tyr	Ser	Lys	Ala	Val	Tyr	Ala	Asn	Asn	Gln
		275					280					285			
Glu	Ser	Ala	Val	Val	Asn	Leu	Ala	Arg	Thr	Asn	Pro	Glu	Gly	Trp	Glu
	290					295					300				
Asn	Asp	Arg	Gly	Pro	Lys	Ile	Glu	Gly	Tyr	Glu	Asp	Ala	Ile	Ile	Tyr
305					310					315					320
Glu	Ile	His	Ile	Ala	Asp	Ile	Thr	Gly	Leu	Glu	Asn	Ser	Gly	Val	Lys
				325					330					335	
Asn	Lys	Gly	Leu	Tyr	Leu	Gly	Leu	Thr	Glu	Glu	Asn	Thr	Lys	Ala	Pro
			340					345					350		
Gly	Gly	Val	Thr	Thr	Gly	Leu	Ser	His	Leu	Val	Glu	Leu	Gly	Val	Thr
		355					360					365			
His	Val	His	Ile	Leu	Pro	Phe	Phe	Asp	Phe	Tyr	Thr	Gly	Asp	Glu	Leu
	370					375					380				
Asp	Lys	Asp	Phe	Glu	Lys	Tyr	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Tyr	Leu
385					390					395					400
Phe	Met	Val	Pro	Glu	Gly	Arg	Tyr	Ser	Thr	Asp	Pro	Lys	Asn	Pro	His
				405					410					415	
Thr	Arg	Ile	Arg	Glu	Val	Lys	Glu	Met	Val	Lys	Ala	Leu	His	Lys	His
			420					425					430		
Gly	Ile	Gly	Val	Ile	Met	Asp	Met	Val	Phe	Pro	His	Thr	Tyr	Gly	Ile
		435				440						445			
Gly	Glu	Leu	Ser	Ala	Phe	Asp	Gln	Thr	Val	Pro	Tyr	Tyr	Phe	Tyr	Arg
	450					455					460				
Ile	Asp	Lys	Thr	Gly	Ala	Tyr	Leu	Asn	Glu	Ser	Gly	Cys	Gly	Asn	Val
465					470					475					480
Ile	Ala	Ser	Glu	Arg	Pro	Met	Met	Arg	Lys	Phe	Ile	Val	Asp	Thr	Val
				485					490					495	
Thr	Tyr	Trp	Val	Lys	Glu	Tyr	His	Ile	Asp	Gly	Phe	Arg	Phe	Asp	Gln
		500						505					510		
Met	Gly	Leu	Ile	Asp	Lys	Lys	Thr	Met	Leu	Glu	Val	Glu	Arg	Ala	Leu
		515					520					525			
His	Lys	Ile	Asp	Pro	Thr	Ile	Ile	Leu	Tyr	Gly	Glu	Pro	Trp	Gly	Gly
	530					535					540				
Trp	Gly	Ala	Pro	Ile	Arg	Phe	Gly	Lys	Ser	Asp	Val	Ala	Gly	Thr	His
545					550					555					560
Val	Ala	Ala	Phe	Asn	Asp	Glu	Phe	Arg	Asp	Ala	Ile	Arg	Gly	Ser	Val
				565					570					575	
Phe	Asn	Pro	Ser	Val	Lys	Gly	Phe	Val	Met	Gly	Gly	Tyr	Gly	Lys	Glu
			580					585					590		
Thr	Lys	Ile	Lys	Arg	Gly	Val	Val	Gly	Ser	Ile	Asn	Tyr	Asp	Gly	Lys
		595				600						605			
Leu	Ile	Lys	Ser	Phe	Ala	Leu	Asp	Pro	Glu	Glu	Thr	Ile	Asn	Tyr	Ala
	610					615					620				
Ala	Cys	His	Asp	Asn	His	Thr	Leu	Trp	Asp	Lys	Asn	Tyr	Leu	Ala	Ala
625					630					635					640

Lys Ala Asp Lys Lys Lys Glu Trp Thr Glu Glu Glu Leu Lys Asn Ala
 645 650 655
 Gln Lys Leu Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe
 660 665 670
 Leu His Gly Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn
 675 680 685
 Ser Tyr Asn Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys
 690 695 700
 Leu Gln Phe Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu
 705 710 715 720
 Arg Lys Glu His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys
 725 730 735
 Lys His Leu Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met
 740 745 750
 Leu Lys Asp His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile
 755 760 765
 Tyr Asn Gly Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys
 770 775 780
 Trp Asn Val Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu
 785 790 795 800
 Thr Val Glu Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu
 805 810 815
 Tyr Arg Glu Ser Glu Lys Asp Glu Leu
 820 825

<210> 25

<211> 2478

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 25

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 gtggccgtgg tgaagctccc gatggacctc accaaggtgg gcatcatcgt gcgcctcaac 180
 gagtggcagg cgaaggacgt ggccaaggac cgcttcacgc agatcaagga cggcaaggcc 240
 gaggtgtgga tactccaggg cgtggaggag atcttctacg agaagccgga cacctccccg 300
 cgcactctct tcgcccaggc ccgctccaac aaggtgatcg aggccttcct caccaaccgc 360
 gtggacacca agaagaagga gctgttcaag gtgaccgtcg acggcaagga gatcccgggtg 420
 tcccgcgtgg agaaggccga cccgaccgac atcgacgtga ccaactacgt gcgcacgtg 480
 ctctccgagt ccctcaagga ggaggacctc cgcaaggacg tggagctgat catcgagggc 540
 tacaagccgg cccgcgtgat catgatggag atcctcgacg actactacta cgacggcgag 600
 ctggggggcg tgtactcccc ggagaagacc atcttccgcg tgtggtcccc ggtgtccaag 660
 tgggtgaagg tgctcctctt caagaacggc gaggacaccg agccgtacca ggtggtgaac 720
 atcgagttaca agggcaacgg cgtgtgggag gccgtggtgg agggcgacct cgacggcggtg 780
 ttctacctct accagctgga gaactacggc aagatccgca ccaccgtgga cccgtactcc 840
 aaggccgtgt acgccaacaa ccaggagtct gcagtgggtg acctcgcccg caccaaccgc 900
 gagggctggg agaacgaccg cggcccgaag atcgagggct acgaggacgc catcatctac 960
 gagatccaca tcgccgacat caccggcctg gagaactccg gcgtgaagaa caagggcctc 1020
 tacctcggcc tcaccgagga gaacaccaag gccccgggcg gcgtgaccac cggcctctcc 1080
 cacctcgtgg agctgggctg gacccacgtg cacatctcc cgcttctcga cttctacacc 1140
 ggcgacgagc tggacaagga cttcgagaag tactacaact ggggctacga cccgtacctc 1200
 ttcattggtg cggaggggcg ctactccacc gaccggaaga acccgcacac ccgaattcgc 1260
 gaggtgaagg agatgggtgaa ggccctccac aagcacggca tcggcgtgat catggacatg 1320
 gtgttccccg acacctacgg catcggcgag ctgtccgcct tcgaccagac cgtgccgtac 1380


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tacttctacc gcatcgacaa gaccggcgcc tacctcaacg agtccggctg cggcaacgtg 1440
atcgccctcc agcgcccgat gatgcgcaag ttcatcgtgg acaccgtgac ctactgggtg 1500
aaggagtlacc acatcgacgg cttccgcttc gaccagatgg gcctcatcga caagaagacc 1560
atgctggagg tggagcgcg cctccacaag atcgacccga ccatcatcct ctacggcgag 1620
ccgtggggcg gctggggggc cccgatccgc ttcggcaagt ccgacgtggc cggcaccac 1680
gtggccqccr tcaacgacga gtcccgcgac gccatccgcg gctccgtgtt caaccgtcc 1740
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ggctccatca actacgacgg caagctcatc aagtccttcg ccctcgaccc ggaggagacc 1860
atcaactacg ccgcctgcca cgacaaccac accctctggg acaagaacta cctcgccgcc 1920
aaggccgaca agaagaagga gtggaccgag gaggagctga agaacgcca gaagctcgcc 1980
ggcgccatcc tcctcactag tcaggggcgtg ccgttctctc acggcgggcca ggacttctgc 2040
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tacgagcgca agctccagtt catcgacgtg ttcaactacc acaagggcct catcaagctc 2160
cgcaaggagc acccggcctt ccgcctcaag aacgcccagg agatcaagaa gcacctggag 2220
ttctctccgg gcgggcgccg catcgtggcc ttcatgctca aggaccacgc cggcggcgac 2280
ccgtggaagg acatcgtggt gatctacaac ggcaacctgg agaagaccac ctacaagctc 2340
ccggagggca agtggaacgt ggtggtgaac tcccagaagg ccggcaccga ggtgatcgag 2400
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<210> 26

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 26

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Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
20      25      30
Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
35      40      45
Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
50      55      60
Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
65      70      75      80
Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
85      90      95
Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
100     105     110
Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
115     120     125
Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
130     135     140
Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
145     150     155     160
Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
165     170     175
Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
180     185     190
Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
195     200     205
Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
210     215     220
Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu

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225					230					235				240	
Phe	Thr	Trp	His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile	Asp
				245					250					255	
Glu	Leu	His	Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His	Gly
			260					265					270		
Ile	Arg	Val	Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly	Lys
		275					280					285			
Phe	Cys	Glu	Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp	Pro
	290					295				300					
Gly	Thr	Thr	Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu	Trp
305					310				315					320	
Trp	Ala	Gly	Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly	Ile
			325					330					335		
Trp	Leu	Asp	Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu	Ile
		340						345				350			
Arg	Asp	Val	Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg	Leu
	355					360					365				
Val	Thr	Thr	Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys	Arg
	370				375				380						
Val	Lys	His	Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala	Met
385				390					395					400	
Ala	Thr	Phe	Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe	Ile
			405					410					415		
Leu	Ser	Arg	Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile	Trp
		420					425					430			
Thr	Gly	Asp	Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu	Gln
	435					440					445				
Leu	Val	Leu	Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys	Asp
	450				455				460						
Ile	Gly	Gly	Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser	Met
465				470				475						480	
Asp	Leu	Leu	Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe	Tyr
		485					490						495		
Arg	Ser	His	Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe	Leu
		500					505					510			
Pro	Asp	Tyr	Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	Val	Glu	Leu	Arg	Tyr
	515					520					525				
Lys	Phe	Leu	Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu	Lys
	530				535				540						
Gly	His	Pro	Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp	Asp
545				550				555						560	
Asp	Met	Tyr	Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu	Leu
		565					570						575		
Tyr	Ala	Pro	Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu	Pro
	580						585					590			
Arg	Gly	Lys	Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly	Lys
	595					600					605				
Ser	Val	Val	Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu	Gly
	610				615				620						
Ser	Ile	Ile	Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu	Thr
625				630				635						640	
Ser	Phe	Lys	Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Ser	Asn	Glu
		645					650						655		
Ile	Lys	Phe	Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr	Ser
	660					665						670			
Glu	Lys	Pro	Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile	Gln
	675					680					685				
Val	Glu	Lys	Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln	Lys

690
 Ile Arg Gly Lys Ile Asn Leu Glu Ser Glu Lys Asp Glu Leu
 705 710 715

<210> 27
 <211> 712
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 27
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
 20 25 30
 Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
 35 40 45
 Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
 50 55 60
 Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
 65 70 75 80
 Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
 85 90 95
 Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
 100 105 110
 Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
 115 120 125
 Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
 130 135 140
 Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
 145 150 155 160
 Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
 165 170 175
 Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
 180 185 190
 Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
 195 200 205
 Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
 210 215 220
 Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu
 225 230 235 240
 Phe Thr Trp His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp
 245 250 255
 Glu Leu His Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly
 260 265 270
 Ile Arg Val Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys
 275 280 285
 Phe Cys Glu Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro
 290 295 300
 Gly Thr Thr Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp
 305 310 315 320
 Trp Ala Gly Leu Ile Ser Glu Trp Leu Ser Gln Gly Val Asp Gly Ile
 325 330 335
 Trp Leu Asp Met Asn Glu Pro Thr Asp Phe Ser Arg Ala Ile Glu Ile
 340 345 350

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Arg Asp Val Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Asp Arg Leu
      355      360      365
Val Thr Thr Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg
      370      375      380
Val Lys His Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met
385      390      395      400
Ala Thr Phe Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile
      405      410      415
Leu Ser Arg Ala Gly Tyr Ala Gly Ile Gln Arg Tyr Ala Phe Ile Trp
      420      425      430
Thr Gly Asp Asn Thr Pro Ser Trp Asp Asp Leu Lys Leu Gln Leu Gln
      435      440      445
Leu Val Leu Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp
      450      455      460
Ile Gly Gly Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met
465      470      475      480
Asp Leu Leu Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr
      485      490      495
Arg Ser His Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu
      500      505      510
Pro Asp Tyr Tyr Lys Glu Lys Val Lys Glu Ile Val Glu Leu Arg Tyr
      515      520      525
Lys Phe Leu Pro Tyr Ile Tyr Ser Leu Ala Leu Glu Ala Ser Glu Lys
      530      535      540
Gly His Pro Val Ile Arg Pro Leu Phe Tyr Glu Phe Gln Asp Asp Asp
545      550      555      560
Asp Met Tyr Arg Ile Glu Asp Glu Tyr Met Val Gly Lys Tyr Leu Leu
      565      570      575
Tyr Ala Pro Ile Val Ser Lys Glu Glu Ser Arg Leu Val Thr Leu Pro
      580      585      590
Arg Gly Lys Trp Tyr Asn Tyr Trp Asn Gly Glu Ile Ile Asn Gly Lys
      595      600      605
Ser Val Val Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly
      610      615      620
Ser Ile Ile Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr
625      630      635      640
Ser Phe Lys Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu
      645      650      655
Ile Lys Phe Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser
      660      665      670
Glu Lys Pro Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln
      675      680      685
Val Glu Lys Thr Met Gln Asn Thr Tyr Val Ala Lys Ile Asn Gln Lys
      690      695      700
Ile Arg Gly Lys Ile Asn Leu Glu
705      710

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<210> 28

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 28

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser

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Ala Thr Ser Met	Ala Glu Phe Phe	Pro Glu Ile Pro	Lys Ile Gln Phe
20	25	30	
Glu Gly Lys Glu	Ser Thr Asn Pro	Leu Ala Phe Arg	Phe Tyr Asp Pro
35	40	45	
Asn Glu Val Ile	Asp Gly Lys Pro	Leu Lys Asp His	Leu Lys Phe Ser
50	55	60	
Val Ala Phe Trp	His Thr Phe Val	Asn Glu Gly Arg	Asp Pro Phe Gly
65	70	75	80
Asp Pro Thr Ala	Glu Arg Pro Trp	Asn Arg Phe Ser	Asp Pro Met Asp
85	90	95	
Lys Ala Phe Ala	Arg Val Asp Ala	Leu Phe Glu Phe	Cys Glu Lys Leu
100	105	110	
Asn Ile Glu Tyr	Phe Cys Phe His	Asp Arg Asp Ile	Ala Pro Glu Gly
115	120	125	
Lys Thr Leu Arg	Glu Thr Asn Lys	Ile Leu Asp Lys	Val Val Glu Arg
130	135	140	
Ile Lys Glu Arg	Met Lys Asp Ser	Asn Val Lys Leu	Leu Trp Gly Thr
145	150	155	160
Ala Asn Leu Phe	Ser His Pro Arg	Tyr Met His Gly	Ala Ala Thr Thr
165	170	175	
Cys Ser Ala Asp	Val Phe Ala Tyr	Ala Ala Gln Val	Lys Lys Ala
180	185	190	
Leu Glu Ile Thr	Lys Glu Leu Gly	Gly Glu Gly Tyr	Val Phe Trp Gly
195	200	205	
Gly Arg Glu Gly	Tyr Glu Thr Leu	Leu Asn Thr Asp	Leu Gly Leu Glu
210	215	220	
Leu Glu Asn Leu	Ala Arg Phe Leu	Arg Met Ala Val	Glu Tyr Ala Lys
225	230	235	240
Lys Ile Gly Phe	Thr Gly Gln Phe	Leu Ile Glu Pro	Lys Pro Lys Glu
245	250	255	
Pro Thr Lys His	Gln Tyr Asp Phe	Asp Val Ala Thr	Ala Tyr Ala Phe
260	265	270	
Leu Lys Asn His	Gly Leu Asp Glu	Tyr Phe Lys Phe	Asn Ile Glu Ala
275	280	285	
Asn His Ala Thr	Leu Ala Gly His	Thr Phe Gln His	Glu Leu Arg Met
290	295	300	
Ala Arg Ile Leu	Gly Lys Leu Gly	Ser Ile Asp Ala	Asn Gln Gly Asp
305	310	315	320
Leu Leu Leu Gly	Trp Asp Thr Asp	Gln Phe Pro Thr	Asn Ile Tyr Asp
325	330	335	
Thr Thr Leu Ala	Met Tyr Glu Val	Ile Lys Ala Gly	Gly Phe Thr Lys
340	345	350	
Gly Gly Leu Asn	Phe Asp Ala Lys	Val Arg Arg Ala	Ser Tyr Lys Val
355	360	365	
Glu Asp Leu Phe	Ile Gly His Ile	Ala Gly Met Asp	Thr Phe Ala Leu
370	375	380	
Gly Phe Lys Ile	Ala Tyr Lys Leu	Ala Lys Asp Gly	Val Phe Asp Lys
385	390	395	400
Phe Ile Glu Glu	Lys Tyr Arg Ser	Phe Lys Glu Gly	Ile Gly Lys Glu
405	410	415	
Ile Val Glu Gly	Lys Thr Asp Phe	Glu Lys Leu Glu	Glu Tyr Ile Ile
420	425	430	
Asp Lys Glu Asp	Ile Glu Leu Pro	Ser Gly Lys Gln	Glu Tyr Leu Glu
435	440	445	
Ser Leu Leu Asn	Ser Tyr Ile Val	Lys Thr Ile Ala	Glu Leu Arg Ser
450	455	460	
Glu Lys Asp Glu	Leu		

465

<210> 29
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<210>
 <223> synthetic

<400> 29
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe
 20 25 30
 Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro
 35 40 45
 Glu Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
 50 55 60
 Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
 65 70 75 80
 Asp Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp
 85 90 95
 Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu
 100 105 110
 Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
 115 120 125
 Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
 130 135 140
 Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
 145 150 155 160
 Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr
 165 170 175
 Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala
 180 185 190
 Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly
 195 200 205
 Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu
 210 215 220
 Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys
 225 230 235 240
 Arg Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
 245 250 255
 Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe
 260 265 270
 Leu Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala
 275 280 285
 Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met
 290 295 300
 Ala Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp
 305 310 315 320
 Leu Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp
 325 330 335
 Thr Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys
 340 345 350
 Gly Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val
 355 360 365

Glu Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu
 370 375 380
 Gly Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys
 385 390 395 400
 Phe Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp
 405 410 415
 Ile Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile
 420 425 430
 Asp Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu
 435 440 445
 Ser Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg Ser
 450 455 460
 Glu Lys Asp Glu Leu
 465

<210> 30
 <211> 463
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 30
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe
 20 25 30
 Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro
 35 40 45
 Glu Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
 50 55 60
 Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
 65 70 75 80
 Asp Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp
 85 90 95
 Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu
 100 105 110
 Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
 115 120 125
 Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
 130 135 140
 Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
 145 150 155 160
 Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr
 165 170 175
 Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Gln Val Lys Lys Ala
 180 185 190
 Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly
 195 200 205
 Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu
 210 215 220
 Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys
 225 230 235 240
 Arg Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
 245 250 255
 Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe

			260					265					270				
Leu	Lys	Ser	His	Gly	Leu	Asp	Glu	Tyr	Phe	Lys	Phe	Asn	Ile	Glu	Ala		
			275					280					285				
Asn	His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	Leu	Arg	Met		
			290					295					300				
Ala	Arg	Ile	Leu	Gly	Lys	Leu	Gly	Ser	Ile	Asp	Ala	Asn	Gln	Gly	Asp		
							310						315				
Leu	Leu	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Thr	Asn	Val	Tyr	Asp		
							325										
Thr	Thr	Leu	Ala	Met	Tyr	Glu	Val	Ile	Lys	Ala	Gly	Gly	Phe	Thr	Lys		
							340										
Gly	Gly	Leu	Asn	Phe	Asp	Ala	Lys	Val	Arg	Arg	Ala	Ser	Tyr	Lys	Val		
							355										
Glu	Asp	Leu	Phe	Ile	Gly	His	Ile	Ala	Gly	Met	Asp	Thr	Phe	Ala	Leu		
							370										
Gly	Phe	Lys	Val	Ala	Tyr	Lys	Leu	Val	Lys	Asp	Gly	Val	Leu	Asp	Lys		
							385										
Phe	Ile	Glu	Glu	Lys	Tyr	Arg	Ser	Phe	Arg	Glu	Gly	Ile	Gly	Arg	Asp		
							405										
Ile	Val	Glu	Gly	Lys	Val	Asp	Phe	Glu	Lys	Leu	Glu	Glu	Tyr	Ile	Ile		
							420										
Asp	Lys	Glu	Thr	Ile	Glu	Leu	Pro	Ser	Gly	Lys	Gln	Glu	Tyr	Leu	Glu		
							435										
Ser	Leu	Ile	Asn	Ser	Tyr	Ile	Val	Lys	Thr	Ile	Leu	Glu	Leu	Arg			
							450										

<210> 31
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 31
 Met Gly Lys Asn Gly Asn Leu Cys Cys Phe Ser Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Ala Gly Leu Ala Ser Gly His Gln
 20 25

<210> 32
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 32
 Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
 1 5 10 15
 Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
 20 25 30

<210> 33

<211> 460
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 33
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Gly Gly Val Ile Met
 20 25 30
 Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
 35 40 45
 Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
 50 55 60
 Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
 65 70 75 80
 Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
 85 90 95
 Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
 100 105 110
 Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
 115 120 125
 Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
 130 135 140
 Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
 145 150 155 160
 Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
 165 170 175
 Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
 180 185 190
 Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
 195 200 205
 Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
 210 215 220
 Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
 225 230 235 240
 Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
 245 250 255
 Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
 260 265 270
 Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
 275 280 285
 Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
 290 295 300
 Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
 305 310 315 320
 Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
 325 330 335
 Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
 340 345 350
 Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
 355 360 365
 Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
 370 375 380
 Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
 385 390 395 400

Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
 405 410 415
 Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
 420 425 430
 Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
 435 440 445
 Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
 450 455 460

<210> 34
 <211> 825
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 34
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Ala Gly His Trp Tyr Lys His Gln Arg Ala Tyr Gln Phe
 20 25 30
 Thr Gly Glu Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met
 35 40 45
 Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
 50 55 60
 Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
 65 70 75 80
 Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
 85 90 95
 Asp Thr Ser Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val
 100 105 110
 Ile Glu Ala Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu
 115 120 125
 Phe Lys Val Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu
 130 135 140
 Lys Ala Asp Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val
 145 150 155 160
 Leu Ser Glu Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu
 165 170 175
 Ile Ile Glu Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu
 180 185 190
 Asp Asp Tyr Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu
 195 200 205
 Lys Thr Ile Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val
 210 215 220
 Leu Leu Phe Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn
 225 230 235 240
 Met Glu Tyr Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp
 245 250 255
 Leu Asp Gly Val Phe Tyr Leu Tyr Gln Leu Glu Asn Tyr Gly Lys Ile
 260 265 270
 Arg Thr Thr Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln
 275 280 285
 Glu Ser Ala Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu
 290 295 300
 Asn Asp Arg Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr

305					310					315				320
Glu	Ile	His	Ile	Ala	Asp	Ile	Thr	Gly	Leu	Glu	Asn	Ser	Gly	Val
				325					330					335
Asn	Lys	Gly	Leu	Tyr	Leu	Gly	Leu	Thr	Glu	Glu	Asn	Thr	Lys	Ala
			340					345					350	Pro
Gly	Gly	Val	Thr	Thr	Gly	Leu	Ser	His	Leu	Val	Glu	Leu	Gly	Val
		355					360					365		Thr
His	Val	His	Ile	Leu	Pro	Phe	Phe	Asp	Phe	Tyr	Thr	Gly	Asp	Glu
	370					375					380			Leu
Asp	Lys	Asp	Phe	Glu	Lys	Tyr	Tyr	Asn	Trp	Gly	Tyr	Asp	Pro	Tyr
385					390					395				400
Phe	Met	Val	Pro	Glu	Gly	Arg	Tyr	Ser	Thr	Asp	Pro	Lys	Asn	Pro
			405						410					415
Thr	Arg	Ile	Arg	Glu	Val	Lys	Glu	Met	Val	Lys	Ala	Leu	His	Lys
		420						425					430	His
Gly	Ile	Gly	Val	Ile	Met	Asp	Met	Val	Phe	Pro	His	Thr	Tyr	Gly
	435					440						445		Ile
Gly	Glu	Leu	Ser	Ala	Phe	Asp	Gln	Thr	Val	Pro	Tyr	Tyr	Phe	Tyr
	450					455					460			Arg
Ile	Asp	Lys	Thr	Gly	Ala	Tyr	Leu	Asn	Glu	Ser	Gly	Cys	Gly	Asn
465					470					475				480
Ile	Ala	Ser	Glu	Arg	Pro	Met	Met	Arg	Lys	Phe	Ile	Val	Asp	Thr
			485					490						495
Thr	Tyr	Trp	Val	Lys	Glu	Tyr	His	Ile	Asp	Gly	Phe	Arg	Phe	Asp
		500						505					510	Gln
Met	Gly	Leu	Ile	Asp	Lys	Lys	Thr	Met	Leu	Glu	Val	Glu	Arg	Ala
	515						520					525		Leu
His	Lys	Ile	Asp	Pro	Thr	Ile	Ile	Leu	Tyr	Gly	Glu	Pro	Trp	Gly
	530					535					540			Gly
Trp	Gly	Ala	Pro	Ile	Arg	Phe	Gly	Lys	Ser	Asp	Val	Ala	Gly	Thr
545					550					555				560
Val	Ala	Ala	Phe	Asn	Asp	Glu	Phe	Arg	Asp	Ala	Ile	Arg	Gly	Ser
			565					570						575
Phe	Asn	Pro	Ser	Val	Lys	Gly	Phe	Val	Met	Gly	Gly	Tyr	Gly	Lys
		580						585					590	Glu
Thr	Lys	Ile	Lys	Arg	Gly	Val	Val	Gly	Ser	Ile	Asn	Tyr	Asp	Gly
	595						600					605		Lys
Leu	Ile	Lys	Ser	Phe	Ala	Leu	Asp	Pro	Glu	Glu	Thr	Ile	Asn	Tyr
	610					615					620			Ala
Ala	Cys	His	Asp	Asn	His	Thr	Leu	Trp	Asp	Lys	Asn	Tyr	Leu	Ala
625					630					635				640
Lys	Ala	Asp	Lys	Lys	Lys	Glu	Trp	Thr	Glu	Glu	Glu	Leu	Lys	Asn
			645					650						655
Gln	Lys	Leu	Ala	Gly	Ala	Ile	Leu	Leu	Thr	Ser	Gln	Gly	Val	Pro
		660						665					670	Phe
Leu	His	Gly	Gly	Gln	Asp	Phe	Cys	Arg	Thr	Thr	Asn	Phe	Asn	Asp
	675					680					685			Asn
Ser	Tyr	Asn	Ala	Pro	Ile	Ser	Ile	Asn	Gly	Phe	Asp	Tyr	Glu	Arg
	690					695					700			Lys
Leu	Gln	Phe	Ile	Asp	Val	Phe	Asn	Tyr	His	Lys	Gly	Leu	Ile	Lys
705					710					715				720
Arg	Lys	Glu	His	Pro	Ala	Phe	Arg	Leu	Lys	Asn	Ala	Glu	Glu	Ile
			725					730						735
Lys	His	Leu	Glu	Phe	Leu	Pro	Gly	Gly	Arg	Arg	Ile	Val	Ala	Phe
		740						745					750	Met
Leu	Lys	Asp	His	Ala	Gly	Gly	Asp	Pro	Trp	Lys	Asp	Ile	Val	Val
	755						760				765			Ile
Tyr	Asn	Gly	Asn	Leu	Glu	Lys	Thr	Thr	Tyr	Lys	Leu	Pro	Glu	Gly
														Lys

770	775	780
Trp Asn Val Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu		
785	790	795
Thr Val Glu Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu		800
	805	810
Tyr Arg Glu Ser Glu Lys Asp Glu Leu		815
	820	825

<210> 35
 <211> 460
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 35

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser	
1	5 10 15
Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Gly Gly Val Ile Met	
	20 25 30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr	
	35 40 45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile	
	50 55 60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly	
65	70 75 80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly	
	85 90 95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile	
	100 105 110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile	
	115 120 125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp	
	130 135 140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala	
145	150 155 160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly	
	165 170 175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln	
	180 185 190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser	
	195 200 205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala	
	210 215 220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly	
225	230 235 240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser	
	245 250 255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala	
	260 265 270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn	
	275 280 285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val	
	290 295 300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala	
305	310 315 320

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Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
      325      330      335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
      340      345      350
Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
      355      360      365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
      370      375      380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
      385      390      395      400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
      405      410      415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
      420      425      430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
      435      440      445
Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
      450      455      460

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<210> 36
 <211> 718
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

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<400> 36
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
  1      5      10      15
Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
      20      25      30
Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
      35      40      45
Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
      50      55      60
Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
      65      70      75      80
Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
      85      90      95
Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
      100      105      110
Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
      115      120      125
Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
      130      135      140
Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
      145      150      155      160
Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
      165      170      175
Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
      180      185      190
Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
      195      200      205
Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
      210      215      220
Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu

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225					230					235					240
Phe	Thr	Trp	His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile	Asp
				245					250					255	
Glu	Leu	His	Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His	Gly
			260					265					270		
Ile	Arg	Val	Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly	Lys
		275					280					285			
Phe	Cys	Glu	Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp	Pro
	290					295				300					
Gly	Thr	Thr	Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu	Trp
305					310					315				320	
Trp	Ala	Gly	Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly	Ile
				325					330					335	
Trp	Leu	Asp	Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu	Ile
			340					345					350		
Arg	Asp	Val	Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg	Leu
		355					360					365			
Val	Thr	Thr	Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys	Arg
	370					375					380				
Val	Lys	His	Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala	Met
385					390					395				400	
Ala	Thr	Phe	Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe	Ile
				405					410					415	
Leu	Ser	Arg	Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile	Trp
			420				425						430		
Thr	Gly	Asp	Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu	Gln
		435					440					445			
Leu	Val	Leu	Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys	Asp
	450					455				460					
Ile	Gly	Gly	Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser	Met
465					470					475				480	
Asp	Leu	Leu	Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe	Tyr
				485					490					495	
Arg	Ser	His	Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe	Leu
			500					505					510		
Pro	Asp	Tyr	Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	Val	Glu	Leu	Arg	Tyr
		515					520					525			
Lys	Phe	Leu	Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu	Lys
	530					535					540				
Gly	His	Pro	Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp	Asp
545					550					555				560	
Asp	Met	Tyr	Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu	Leu
				565					570					575	
Tyr	Ala	Pro	Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu	Pro
			580					585					590		
Arg	Gly	Lys	Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly	Lys
		595					600					605			
Ser	Val	Val	Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu	Gly
	610					615					620				
Ser	Ile	Ile	Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu	Thr
625					630					635				640	
Ser	Phe	Lys	Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Ser	Asn	Glu
				645					650					655	
Ile	Lys	Phe	Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr	Ser
			660				665						670		
Glu	Lys	Pro	Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile	Gln
	675					680						685			
Val	Glu	Lys	Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln	Lys

690 695 700
 Ile Arg Gly Lys Ile Asn Leu Glu Ser Glu Lys Asp Glu Leu
 705 710 715

<210> 37
 <211> 1434
 <212> DNA
 <213> Thermotoga maritima

<400> 37
 atgaaagaaa ccgctgctgc taaattcgaa cgccagcaca tggacagccc agatctgggt 60
 accctggtgc cagcggttc catggccgag ttcttcccgg agatcccga gatccagttc 120
 gagggcaagg agtccacca cccgctcgcc ttccgcttct acgaccgaa cgaggtgatc 180
 gacggcaagc cgctcaagga ccacctcaag ttctccgtgg ccttctggca caccttcgtg 240
 aacgagcgcc gcgaccggt cggcgacccg accgccgagc gcccgaggaa ccgcttctcc 300
 gacccgatgg acaaggcctt cgcccgcgtg gacgccctct tcgagttctg cgagaagctc 360
 aacatcgagt acttctgctt ccacgaccgc gacatcgccc cggaggggcaa gaccctccgc 420
 gagaccaaca agatcctcga caaggtggtg gagcgcatca aggagcgcat gaaggactcc 480
 aacgtgaagc tcctctgggg caccgccaac ctcttctccc acccgcgcta catgcacggc 540
 gccgccacca cctgctccgc cgacgtgttc gcctacgccg ccgcccaggt gaagaaggcc 600
 ctggagatca ccaaggagct gggcggcgag ggctacgtgt tctggggcgg ccgcgagggc 660
 tacgagacct tcctcaacac cgacctcggc ctggagctgg agaacctcgc ccgcttctc 720
 cgcattggccg tggagtacgc caagaagatc ggcttcaccg gccagttcct catcgagccg 780
 aagccgaagg agccgaccaa gcaccagtac gacttcgacg tggccaccgc ctacgccttc 840
 ctcaagaacc acggcctcga cgagtacttc aagttcaaca tcgaggccaa ccacgccacc 900
 ctgcgcggcc acaccttcca gcacgagctg cgcattggccc gcatcctcgg caagctcggc 960
 tccatcgacg ccaaccaggg cgacctcttc ctcggtggg acaccgacca gttcccgacc 1020
 aacatctacg acaccacct cgccatgtac gaggtgatca aggcggcgcg cttaccaag 1080
 ggcggcctca acttcgacgc caaggtgcgc cgcgcctcct acaaggtgga ggacctcttc 1140
 atcgccaca tcgcccgcgt ggacaccttc gccctcggct tcaagatcgc ctacaagctc 1200
 gccaaaggac gcgtgttcga caagttcatc gaggagaagt accgctcctt caaggagggc 1260
 atcggaagg agatcgtgga gggcaagacc gacttcgaga agctggagga gtacatcatc 1320
 gacaaggagg acatcgagct gccgtccggc aagcaggagt acctggagtc cctcctcaac 1380
 tcctacatcg tgaagaccat cgccgagctg cgctccgaga aggacgagct gtga 1434

<210> 38
 <211> 477
 <212> PRT
 <213> Thermotoga maritima

<400> 38
 Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
 1 5 10 15
 Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Met Ala Glu Phe Phe
 20 25 30
 Pro Glu Ile Pro Lys Ile Gln Phe Glu Gly Lys Glu Ser Thr Asn Pro
 35 40 45
 Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val Ile Asp Gly Lys Pro
 50 55 60
 Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe Trp His Thr Phe Val
 65 70 75 80
 Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr Ala Glu Arg Pro Trp
 85 90 95
 Asn Arg Phe Ser Asp Pro Met Asp Lys Ala Phe Ala Arg Val Asp Ala
 100 105 110
 Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu Tyr Phe Cys Phe His
 115 120 125

Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu Arg Glu Thr Asn Lys
 130 135 140
 Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu Arg Met Lys Asp Ser
 145 150 155 160
 Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu Phe Ser His Pro Arg
 165 170 175
 Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
 180 185 190
 Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile Thr Lys Glu Leu Gly
 195 200 205
 Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
 210 215 220
 Leu Asn Thr Asp Leu Gly Leu Glu Leu Glu Asn Leu Ala Arg Phe Leu
 225 230 235 240
 Arg Met Ala Val Glu Tyr Ala Lys Lys Ile Gly Phe Thr Gly Gln Phe
 245 250 255
 Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys His Gln Tyr Asp Phe
 260 265 270
 Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Asn His Gly Leu Asp Glu
 275 280 285
 Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala Thr Leu Ala Gly His
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 Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu Asp Ile Glu Leu Pro
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35      40      45
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50      55      60
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85      90      95
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Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
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195     200     205
Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
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225     230     235     240
Arg Met Ala Val Asp Tyr Ala Lys Arg Ile Gly Phe Thr Gly Gln Phe
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Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys His Gln Tyr Asp Phe

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Page 43

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 385 390 395 400
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Phe Asp Lys Ser Asp Gly Asp Glu Leu Ser Ala Arg Asp Leu Thr Trp		875
	885	890
Ser Tyr Ala Ala Leu Leu Thr Ala Asn Asn Arg Arg Asn Ser Val Val		895
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<211> 679

<212> PRT

<213> Thermoanaerobacterium thermosaccharolyticum

<400> 47

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Pro Thr Ile Asp Thr Ala Asp Val Lys Glu Ile Lys Phe Ile Val Thr
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Asp Gly Lys Ser Phe Val Ser Asp Glu Thr Lys Asp Ala Ile Ser Lys
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caggcggtgg gcggccccgc cgcggcgctc gacttcacca ccaagggcgt gctgcaggcg 840
gccgtccagg gcgagctgtg gcgcatgaag gacggcaacg gcaaggcgcc cgggatgatc 900
ggctggctgc cggagaaggc cgtcacgttc gtcgacaacc acgacaccgg ctccacgcag 960
aactcgtggc cattccccct cgacaaggct atgcagggct acgectatat cctcacgcac 1020
ccaggaaetc catgcatctt ctacgaccac gttttcgact ggaacctgaa gcaggagatc 1080
agcgcgctgt ctgcggtgag gtcaagaaac gggatccacc cggggagcga gctgaacatc 1140
ctcgccgccg acgggggatct ctacgtcgcc aagattgacg acaaggtcat cgtgaagatc 1200
gggtcacggt acgacgtcgg gaacctgac ccctcagact tccacgccgt tgccctggc 1260
aacaactact gcgtttggga gaagcacggt ctgagagttc cagcggggcg gcaccactag 1320

<210> 53
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 53
Ala Thr Gly Gly Thr Thr Thr Thr Ala Thr Thr Thr Gly Ser Gly Gly
1 5 10 15
Val Thr Ser Thr Ser Lys Thr Thr Thr Thr Ala Ser Lys Thr Ser Thr
20 25 30
Thr Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val
35 40 45

<210> 54
<211> 137
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 54

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gccaccggcg gcaccaccac caccgccacc accaccggct cggcgggcgt gacctccacc 60
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accccgaccg ccgtgtc                                     137

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<210> 55

<211> 300

<212> PRT

<213> *Pyrococcus furiosus*

<400> 55

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Ile Tyr Phe Val Glu Lys Tyr His Thr Ser Glu Asp Lys Ser Thr Ser
1      5      10      15
Asn Thr Ser Ser Thr Pro Pro Gln Thr Thr Leu Ser Thr Thr Lys Val
20      25      30
Leu Lys Ile Arg Tyr Pro Asp Asp Gly Glu Trp Pro Gly Ala Pro Ile
35      40      45
Asp Lys Asp Gly Asp Gly Asn Pro Glu Phe Tyr Ile Glu Ile Asn Leu
50      55      60
Trp Asn Ile Leu Asn Ala Thr Gly Phe Ala Glu Met Thr Tyr Asn Leu
65      70      75      80
Thr Ser Gly Val Leu His Tyr Val Gln Gln Leu Asp Asn Ile Val Leu
85      90      95
Arg Asp Arg Ser Asn Trp Val His Gly Tyr Pro Glu Ile Phe Tyr Gly
100      105      110
Asn Lys Pro Trp Asn Ala Asn Tyr Ala Thr Asp Gly Pro Ile Pro Leu
115      120      125
Pro Ser Lys Val Ser Asn Leu Thr Asp Phe Tyr Leu Thr Ile Ser Tyr
130      135      140
Lys Leu Glu Pro Lys Asn Gly Leu Pro Ile Asn Phe Ala Ile Glu Ser
145      150      155      160
Trp Leu Thr Arg Glu Ala Trp Arg Thr Thr Gly Ile Asn Ser Asp Glu
165      170      175
Gln Glu Val Met Ile Trp Ile Tyr Tyr Asp Gly Leu Gln Pro Ala Gly
180      185      190
Ser Lys Val Lys Glu Ile Val Val Pro Ile Ile Val Asn Gly Thr Pro
195      200      205
Val Asn Ala Thr Phe Glu Val Trp Lys Ala Asn Ile Gly Trp Glu Tyr
210      215      220
Val Ala Phe Arg Ile Lys Thr Pro Ile Lys Glu Gly Thr Val Thr Ile
225      230      235      240
Pro Tyr Gly Ala Phe Ile Ser Val Ala Ala Asn Ile Ser Ser Leu Pro
245      250      255
Asn Tyr Thr Glu Leu Tyr Leu Glu Asp Val Glu Ile Gly Thr Glu Phe
260      265      270
Gly Thr Pro Ser Thr Thr Ser Ala His Leu Glu Trp Trp Ile Thr Asn
275      280      285
Ile Thr Leu Thr Pro Leu Asp Arg Pro Leu Ile Ser
290      295      300

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<210> 56

<211> 903

<212> DNA

<213> *Pyrococcus furiosus*

<400> 56

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atctacttcg tggagaagta ccacacctcc gaggacaagt ccacctccaa cacctcctcc 60
accccgccgc agaccaccct ctccaccacc aaggtgctca agatccgcta cccggacgac 120
ggcgagtggc ccggcgcccc gatcgacaag gacggcgacg gcaacccgga gttctacatc 180
gagatcaacc tctggaacat cctcaacgcc accggcttcg ccgagatgac ctacaacctc 240
actagtggcg tgctccacta cgtgcagcag ctcgacaaca tcgtgctccg cgaccgctcc 300
aactgggtgc acggctaccc ggaaatcttc tacggcaaca agccgtggaa cgccaactac 360
gccaccgacg gcccgatccc gctcccgtcc aaggtgtcca acctcaccga cttctacctc 420
accatctcct acaagctcga gccgaagaac ggtctcccga tcaacttcgc catcgagtcc 480
tggctcaccg gcgaggcctg gcgcaccacc ggcataaact ccgacgagca ggaggtgatg 540
atctggatct actacgacgg cctccagccc gcgggctcca aggtgaagga gatcgtgggtg 600
ccgatcatcg tgaacggcac cccgggtgaac gccaccttcg aggtgtggaa ggccaacatc 660
ggctgggagt acgtggcctt ccgcataaag accccgatca aggagggcac cgtgaccatc 720
ccgtacggcg ccttcattct cgtggccgcc aacatctcct ccctcccgaa ctacaccgag 780
aagtacctcg aggacgtgga gatcggcacc gagttcggca ccccgctccac cacctccgcc 840
cacctcgagt ggtggatcac caacatcacc ctacccccgc tcgaccgccc gctcatctcc 900
tag 903

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<210> 57

<211> 387

<212> PRT

<213> *Thermus flavus*

<400> 57

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Met Tyr Glu Pro Lys Pro Glu His Arg Phe Thr Phe Gly Leu Trp Thr
1      5      10
Val Asp Asn Val Asp Arg Asp Pro Phe Gly Asp Thr Val Arg Glu Arg
20     25     30
Leu Asp Pro Val Tyr Val Val His Lys Leu Ala Glu Leu Gly Ala Tyr
35     40     45
Gly Val Asn Leu His Asp Glu Asp Leu Ile Pro Arg Gly Thr Pro Pro
50     55     60
Gln Glu Arg Asp Gln Ile Val Arg Arg Phe Lys Lys Ala Leu Asp Glu
65     70     75     80
Thr Val Leu Lys Val Pro Met Val Thr Ala Asn Leu Phe Ser Glu Pro
85     90     95
Ala Phe Arg Asp Gly Ala Ser Thr Thr Arg Asp Pro Trp Val Trp Ala
100    105    110
Tyr Ala Leu Arg Lys Ser Leu Glu Thr Met Asp Leu Gly Ala Glu Leu
115    120    125
Gly Ala Glu Ile Tyr Met Phe Trp Met Val Arg Glu Arg Ser Glu Val
130    135    140
Glu Ser Thr Asp Lys Thr Arg Lys Val Trp Asp Trp Val Arg Glu Thr
145    150    155    160
Leu Asn Phe Met Thr Ala Tyr Thr Glu Asp Gln Gly Tyr Gly Tyr Arg
165    170    175
Phe Ser Val Glu Pro Lys Pro Asn Glu Pro Arg Gly Asp Ile Tyr Phe
180    185    190
Thr Thr Val Gly Ser Met Leu Ala Leu Ile His Thr Leu Asp Arg Pro
195    200    205
Glu Arg Phe Gly Leu Asn Pro Glu Phe Ala His Glu Thr Met Ala Gly
210    215    220
Leu Asn Phe Asp His Ala Val Ala Gln Ala Val Asp Ala Gly Lys Leu
225    230    235    240
Phe His Ile Asp Leu Asn Asp Gln Arg Met Ser Arg Phe Asp Gln Asp
245    250    255
Leu Arg Phe Gly Ser Glu Asn Leu Lys Ala Gly Phe Phe Leu Val Asp
260    265    270

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Leu Leu Glu Ser Ser Gly Tyr Gln Gly Pro Arg His Phe Glu Ala His
 275 280 285
 Ala Leu Arg Thr Glu Asp Glu Glu Gly Val Trp Thr Phe Val Arg Val
 290 295 300
 Cys Met Arg Thr Tyr Leu Ile Ile Lys Val Arg Ala Glu Thr Phe Arg
 305 310 315 320
 Glu Asp Pro Glu Val Lys Glu Leu Leu Ala Tyr Tyr Gln Glu Asp
 325 330 335
 Pro Ala Thr Leu Ala Leu Leu Asp Pro Tyr Ser Arg Glu Lys Ala Glu
 340 345 350
 Ala Leu Lys Arg Ala Glu Leu Pro Leu Glu Thr Lys Arg Arg Arg Gly
 355 360 365
 Tyr Ala Leu Glu Arg Leu Asp Gln Leu Ala Val Glu Tyr Leu Leu Gly
 370 375 380
 Val Arg Gly
 385

<210> 58
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 58
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 gcgctccggcc atcaaatcta ctctgtggag aagtaccaca cctccgagga caagtccacc 120
 tccaacacct cctccacccc gccgcagacc accctctcca ccaccaaggt gctcaagatc 180
 cgctaccggg acgacgggtga gtggcccggc gccccgatcg acaaggacgg cgacggcaac 240
 ccggagttct acatcgagat caacctctgg aacatcctca acgccaccgg ctctgccgag 300
 atgacctaca acctcactag tggcgtgctc cactacgtgc agcagctcga caacatcgtg 360
 ctccgcgacc gctccaactg ggtgcacggc taccggaaa tcttctacgg caacaagccg 420
 tggaaagcca actacgccac cgaacggccc atcccgtcc cgtccaaggt gtccaacctc 480
 accgacttct acctcaccat ctctacaag ctcgagccga agaacgggtc cccgatcaac 540
 ttccgcatcg agtccctggt caccgcgag gcctggcgca ccaccggcat caactccgac 600
 gagcaggagg tgatgatctg gatctactac gacggcctcc agcccgcggg ctccaaggtg 660
 aaggagatcg tggtgccgat catcgtgaac ggcaccccg tgaacgccac ctctgaggtg 720
 tggaaagcca acatcggctg ggagtagctg gccttccgca tcaagacccc gatcaaggag 780
 ggcaccgtga ccataccgta cggcgccctt atctccgtgg ccgccaacat ctctctcctc 840
 ccgaactaca ccgagaagta cctcgaggac gtggagatcg gcaccgagtt cggcaccgcc 900
 tccaccacct ccgcccacct cgagtgggtg atcaccaaca tcaccctcac cccgctcgac 960
 cgcccgctca tctcctag 978

<210> 59
 <211> 1920
 <212> DNA
 <213> *Aspergillus niger*

<400> 59
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 atctccaagc gcgccacct cgactcctgg ctctccaacg aggccaccgt ggcccgcacc 120
 gccatcttca acaacatcgg cgccgacggc gcctgggtgt ccggcgccga ctccggcatc 180
 gtggtggcct ccccgctccac cgacaacccg gactacttct acacctggac ccgcgactcc 240
 ggcctcgtgc tcaagacct cgtggacctc ttccgcaacg gcgacacctc cctcctctcc 300
 accatcgaga actacatctc cgcccaggcc atcgtgcagg gcattctcaa cccgtccggc 360
 gacctctcct ccggcgccgg cctcggcgag ccgaagttca acgtggacga gaccgcctac 420

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accggctcct ggggcccggc gcagcgcgac ggcccggccc tccgcgccac cgccatgac 480
ggcttcggcc agtggctcct cgacaacggc tacacctcca ccgccaccga catcgtgtgg 540
ccgctcgtgc gcaacgacct ctctacgtg gccagtagt ggaaccagac cggctacgac 600
ctctgggagg aggtgaacgg ctctccttc ttcaccatcg ccgtgcagca ccgcgcctc 660
gtggagggtt ccgccttcgc caccgccgtg ggctcctcct gctcctggtg cgactcccag 720
gccccggaga tctctgcta cctccagtc ttctggaccg gctccttcac cctcgccaac 780
ttcgactcct ccgctccgg caaggacgcc aacacctcc tcggctccat ccacacctc 840
gaccggagg ccgcctgcga cgactccacc ttccagccgt gctccccgcg cgccctcgc 900
aaccacaagg aggtgggtgga ctcttccgc tccatctaca cctcaacga cggcctctc 960
gactccgagg ccgtggccgt gggccgctac ccggaggaca cctactaaa cggcaaccgc 1020
tggttcctct gcacctcgc cggcgcgag cagctctacg acgacctcta ccagtgggac 1080
aagcagggtt cctcagagg gaccgacgtg tccctcgact tcttcaaggc cctctactc 1140
gacgcccga ccggcaccta ctctcctcc tctccacct actcctccat cgtggacgc 1200
gtgaagacct tcgcccagcg ctctcgtgac atcgtggaga cccacgcgc ctccaacgc 1260
tccatgtccg agcagtaga caagtccgac ggcgagcagc tctccgcccg cgacctcac 1320
tggtcctacg ccgcctcct caccgccaac aaccgcccga actccgtgt gccggcctc 1380
tgggggcaga cctccgcctc ctccgtgccg ggcacctgc ccgccacct cgccatcgc 1440
acctactcct ccgtgaccgt gacctcctgg ccgtccatcg tggccaccg cggcaccac 1500
accaccgca ccccgaccgg ctccggctcc gtgacctcca cctccaagac caccgccac 1560
gcctccaaga cctccacctc cactcctcc acctcctgca ccaccccgac cgccgtggc 1620
gtgaccttcg acctcaccgc caccaccacc tacggcgaga acatctacct cgtgggctc 1680
atctcccagc tcggcgactg ggagacctcc gacggcatcg cctctccgc cgacaagtac 1740
acctcctccg acccgctctg gtacgtgacc gtgacctcc cggccggcga gtccttcgag 1800
tacaagttca tccgcatcga gtccgacgac tccgtggagt gggagtccga cccgaaccgc 1860
gagtagaccg tggcgaggc ctgcggcacc tccaccgca ccgtgaccga cactggcgc 1920

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<210> 60
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 60
 Ser Glu Lys Asp Glu Leu
 1 5

<210> 61
 <211> 561
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Xylanase BD7436

<220>
 <221> CDS
 <222> (1)..(561)

<400> 61
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 Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr
 1 5 10 15

gtg aac gct acc aac ggc agc gac ggc aac tac agc gtg agc tgg agc 96
 Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30

 aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc agc gct 144
 Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45

 acc agg gtg atc aac tac aac gct cat gct ttc agc gtg gtg ggc aac 192
 Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn
 50 55 60

 gct tac ttg gct ttg tac ggc tgg acc agg aac agc ttg atc gag tac 240
 Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80

 tac gtg gtg gac agc tgg ggc acc tac agg cca acc ggc acc tac aag 288
 Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95

 ggc acc gtg acc agc gac ggc ggc acc tac gac atc tac acc acc acc 336
 Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110

 agg acc aac gct cca agc atc gac ggc aac aac acc acc ttc acc caa 384
 Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125

 ttc tgg agc gtg agg caa agc aag agg cca atc ggc acc aac aac acc 432
 Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140

 atc acc ttc agc aac cat gtg aac gct tgg aag agc aag ggc atg aac 480
 Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160

 ttg ggc agc agc tgg agc tac caa gtg ttg gct acc gag ggc tac caa 528
 Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175

 agc agc ggc tac agc aac gtg acc gtg tgg tag 561
 Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

<210> 62
 <211> 186
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 62

Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr
 1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn
50 55 60

Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

<210> 63
<211> 561
<212> DNA
<213> Artificial Sequence

<220>
<223> Xylanase BD6002A

<220>
<221> CDS
<222> (1)..(561)

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<400> 63
atg gct agc acc gac tac tgg caa aac tgg acc gac ggc ggc ggc acc 48
Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
1 5 10 15

gtg aac gct acc aac ggc agc gac ggc aac tac agc gtg agc tgg agc 96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc agc gct 144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

acc agg gtg atc aac tac aac gct ggc gct ttc agc cca agc ggc aac 192
Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50 55 60

ggc tac ttg gct ttg tac ggc tgg acc agg aac agc ttg atc gag tac 240
Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

tac gtg gtg gac agc tgg ggc acc tac agg cca acc ggc acc tac aag 288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

ggc acc gtg acc agc gac ggc ggc acc tac gac atc tac acc acc acc 336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

agg acc aac gct cca agc atc gac ggc aac aac acc acc ttc acc caa 384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

ttc tgg agc gtg agg caa agc aag agg cca atc ggc acc aac aac acc 432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

atc acc ttc agc aac cat gtg aac gct tgg aag agc aag ggc atg aac 480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

ttg ggc agc agc tgg agc tac caa gtg ttg gct acc gag ggc tac caa 528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

agc agc ggc tac agc aac gtg acc gtg tgg tag 561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

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<210> 64
<211> 186
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Construct

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<400> 64

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
 1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
 50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

<210> 65

<211> 561

<212> DNA

<213> Artificial Sequence

<220>

<223> Xylanase BD6002B

<220>

<221> CDS

<222> (1) .. (561)

<400> 65

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Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr	
1 5 10 15	
gtg aac gcc acc aac ggc tcc gac ggc aac tac tcc gtg tcc tgg tcc	96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser	
20 25 30	
aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc tcc gcc	144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala	
35 40 45	
acc cgc gtg atc aac tac aac gcc ggc gcc ttc tcc ccg tcc ggc aac	192
Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn	
50 55 60	
ggc tac ctc gcc ctc tac ggc tgg acc cgc aac tcc ctc atc gag tac	240
Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr	
65 70 75 80	
tac gtg gtg gac tcc tgg ggc acc tac cgc ccg acc ggc acc tac aag	288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys	
85 90 95	
ggc acc gtg acc tcc gac ggc ggc acc tac gac atc tac acc acc acc	336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr	
100 105 110	
cgc acc aac gcc ccg tcc atc gac ggc aac aac acc acc ttc acc cag	384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln	
115 120 125	
ttc tgg tcc gtg cgc cag tcc aag cgc ccg atc ggc acc aac aac acc	432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr	
130 135 140	
atc acc ttc tcc aac cac gtg aac gcc tgg aag tcc aag ggc atg aac	480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn	
145 150 155 160	
ctc ggc tcc tcc tgg tcc tac cag gtg ctc gcc acc gag ggc tac cag	528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln	
165 170 175	
tcc tcc ggc tac tcc aac gtg acc gtg tgg tga	561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp	
180 185	

<210> 66

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 66

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
 1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
 50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

<210> 67

<211> 2071

<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<222> (1)..(2071)
<223> Promoter

<400> 67
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ctaaccatca acaacatgaa atgcttatga ggcctttgct gagcagccaa tcttgccctg 180
gtttatgtct tcacaggccg aattcctctg ttttgttttt caccctcaat atttggaaac 240
atttatctag gttgtttgtg tccaggccta taaatcatac atgatgttgt cgtattggat 300
gtgaatgtgg tggcgtgttc agtgccctgg atttgagttt gatgagagtt gcttctgggt 360
caccactcac cattatcgat gctcctcttc agcataaggt aaaagtcttc cctgtttacg 420
ttattttacc cactatgggt gcttgggttg gttttttcct gattgcttat gccatggaaa 480
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catgagcaat agtggttgca tgatatttag gctgcattcg tttactctct tgatttccat 840
gagcacgctt cccaaactgt taaactctgt gttttttgcc aaaaaaaaaat gcataggaaa 900
gttgctttta aaaaatcata tcaatccatt ttttaagtta tagctaatac ttaattaatc 960
atgcgctaac aagtcactct gtttttcgta ctagagagat tgttttgaac cagcactcaa 1020
gaacacagcc ttaaccacgc caaataatgc tacaacctac cagtccacac ctcttgtaaa 1080
gcatttggtg catggaaaag ctaagatgac agcaacctgt tcaggaaaac aactgacaag 1140
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taatgaaaga agatgtggtg ttagaaaagg aaacaatatc atgagtaatg tgtgggcatt 1380
atgggaccac gaaataaaaa gaacattttg atgagtcgtg taccctcgat gagcctcaaa 1440

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agttctctca ccccgataa gaaaccctta agcaatgtgc aaagtttgca ttctccactg 1500
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tctcaacctt ttcattccta ctcatctaca taagtatctt cagctaaatg ttagaacata 1620
aaccataag tcacgtttga tgagtattag gcgtgacaca tgacaaatca cagactcaag 1680
caagataaag caaaatgatg tgtacataaa actccagagc tatatgtcat attgcaaaaa 1740
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agaggagggc ttacattat ccattgtcata ttgcaaaaga aagagagaaa gaacaacaca 1860
atgctgcgtc aattatacat atctgtatgt ccattcattat tcattccact ttcgtgtacc 1920
acatttcata tatcatgagt cacttcattg ctggacatta acaaaactta tcttaacatt 1980
tagatgcaag agcctttatc tcaactataaa tgcacgatga tttctcattg tttctcacia 2040
aaagcattca gttcattagt cctacaacaa c 2071

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<210> 68
<211> 79
<212> PRT
<213> Zea mays

```

```

<220>
<221> SIGNAL
<222> (1)..(79)
<223> Maize waxy signal sequence.

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<400> 68

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Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1          5          10          15

```

```

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
20          25          30

```

```

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
35          40          45

```

```

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
50          55          60

```

```

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala
65          70          75

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```

<210> 69
<211> 1005

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<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Bromelain Sequence

<220>
 <221> CDS
 <222> (1)..(1005)
 <223> Synthetic Bromelain

<400> 69
 atg gcc tgg aag gtg cag gtg gtg ttc ctc ttc ctc ttc ctc tgc gtg 48
 Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
 1 5 10 15

atg tgg gcc tcc ccg tcc gcc gcc tcc gcg gac gag ccg tcc gac ccg 96
 Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
 20 25 30

atg atg aag cgc ttc gag gag tgg atg gtg gag tac ggc cgc gtg tac 144
 Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
 35 40 45

aag gac aac gac gag aag atg cgc cgc ttc cag atc ttc aag aac aac 192
 Lys Asp Asn Asp Glu Lys Met Arg Arg Phe Gln Ile Phe Lys Asn Asn
 50 55 60

gtg aac cac atc gag acc ttc aac tcc cgc aac gag aac tcc tac acc 240
 Val Asn His Ile Glu Thr Phe Asn Ser Arg Asn Glu Asn Ser Tyr Thr
 65 70 75 80

ctc ggc atc aac cag ttc acc gac atg acc aac aac gag ttc atc gcc 288
 Leu Gly Ile Asn Gln Phe Thr Asp Met Thr Asn Asn Glu Phe Ile Ala
 85 90 95

cag tac acc ggc ggc atc tcc cgc ccg ctc aac atc gag cgc gag ccg 336
 Gln Tyr Thr Gly Gly Ile Ser Arg Pro Leu Asn Ile Glu Arg Glu Pro
 100 105 110

gtg gtg tcc ttc gac gac gtg gac atc tcc gcc gtg ccg cag tcc atc 384
 Val Val Ser Phe Asp Asp Val Asp Ile Ser Ala Val Pro Gln Ser Ile
 115 120 125

gac tgg cgc gac tac ggc gcc gtg acc tcc gtg aag aac cag aac ccg 432
 Asp Trp Arg Asp Tyr Gly Ala Val Thr Ser Val Lys Asn Gln Asn Pro
 130 135 140

tgc ggc gcc tgc tgg gcc ttc gcc gcc atc gcc acc gtg gag tcc atc 480
 Cys Gly Ala Cys Trp Ala Phe Ala Ala Ile Ala Thr Val Glu Ser Ile
 145 150 155 160

tac aag atc aag aag ggc atc ctc gag ccg ctc tcc gag cag cag gtg 528
 Tyr Lys Ile Lys Lys Gly Ile Leu Glu Pro Leu Ser Glu Gln Gln Val
 165 170 175

ctc gac tgc gcc aag ggc tac ggc tgc aag ggc ggc tgg gag ttc cgc 576

Leu Asp Cys Ala Lys Gly Tyr Gly Cys Lys Gly Gly Trp Glu Phe Arg
 180 185 190
 gcc ttc gag ttc atc atc tcc aac aag ggc gtg gcc tcc ggc gcc atc 624
 Ala Phe Glu Phe Ile Ile Ser Asn Lys Gly Val Ala Ser Gly Ala Ile
 195 200 205
 tac ccg tac aag gcc gcc aag ggc acc tgc aag acc gac ggc gtg ccg 672
 Tyr Pro Tyr Lys Ala Ala Lys Gly Thr Cys Lys Thr Asp Gly Val Pro
 210 215 220
 aac tcc gcc tac atc acc ggc tac gcc cgc gtg ccg cgc aac aac gag 720
 Asn Ser Ala Tyr Ile Thr Gly Tyr Ala Arg Val Pro Arg Asn Asn Glu
 225 230 235 240
 tcc tcc atg atg tac gcc gtg tcc aag cag ccg atc acc gtg gcc gtg 768
 Ser Ser Met Met Tyr Ala Val Ser Lys Gln Pro Ile Thr Val Ala Val
 245 250 255
 gac gcc aac gcc aac ttc cag tac tac aag tcc ggc gtg ttc aac ggc 816
 Asp Ala Asn Ala Asn Phe Gln Tyr Tyr Lys Ser Gly Val Phe Asn Gly
 260 265 270
 ccg tgc ggc acc tcc ctc aac cac gcc gtg acc gcc atc ggc tac ggc 864
 Pro Cys Gly Thr Ser Leu Asn His Ala Val Thr Ala Ile Gly Tyr Gly
 275 280 285
 cag gac tcc atc atc tac ccg aag aag tgg ggc gcc aag tgg ggc gag 912
 Gln Asp Ser Ile Ile Tyr Pro Lys Lys Trp Gly Ala Lys Trp Gly Glu
 290 295 300
 gcc ggc tac atc cgc atg gcc cgc gac gtg tcc tcc tcc tcc ggc atc 960
 Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
 305 310 315 320
 tgc ggc atc gcc atc gac ccg ctc tac ccg acc ctc gag gag tag 1005
 Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
 325 330

<210> 70
 <211> 334
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 70

Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
 1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
 20 25 30

Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
 35 40 45
 Lys Asp Asn Asp Glu Lys Met Arg Arg Phe Gln Ile Phe Lys Asn Asn
 50 55 60
 Val Asn His Ile Glu Thr Phe Asn Ser Arg Asn Glu Asn Ser Tyr Thr
 65 70 75 80
 Leu Gly Ile Asn Gln Phe Thr Asp Met Thr Asn Asn Glu Phe Ile Ala
 85 90 95
 Gln Tyr Thr Gly Gly Ile Ser Arg Pro Leu Asn Ile Glu Arg Glu Pro
 100 105 110
 Val Val Ser Phe Asp Asp Val Asp Ile Ser Ala Val Pro Gln Ser Ile
 115 120 125
 Asp Trp Arg Asp Tyr Gly Ala Val Thr Ser Val Lys Asn Gln Asn Pro
 130 135 140
 Cys Gly Ala Cys Trp Ala Phe Ala Ala Ile Ala Thr Val Glu Ser Ile
 145 150 155 160
 Tyr Lys Ile Lys Lys Gly Ile Leu Glu Pro Leu Ser Glu Gln Gln Val
 165 170 175
 Leu Asp Cys Ala Lys Gly Tyr Gly Cys Lys Gly Gly Trp Glu Phe Arg
 180 185 190
 Ala Phe Glu Phe Ile Ile Ser Asn Lys Gly Val Ala Ser Gly Ala Ile
 195 200 205
 Tyr Pro Tyr Lys Ala Ala Lys Gly Thr Cys Lys Thr Asp Gly Val Pro
 210 215 220
 Asn Ser Ala Tyr Ile Thr Gly Tyr Ala Arg Val Pro Arg Asn Asn Glu
 225 230 235 240
 Ser Ser Met Met Tyr Ala Val Ser Lys Gln Pro Ile Thr Val Ala Val
 245 250 255
 Asp Ala Asn Ala Asn Phe Gln Tyr Tyr Lys Ser Gly Val Phe Asn Gly
 260 265 270

Pro Cys Gly Thr Ser Leu Asn His Ala Val Thr Ala Ile Gly Tyr Gly
275 280 285

Gln Asp Ser Ile Ile Tyr Pro Lys Lys Trp Gly Ala Lys Trp Gly Glu
290 295 300

Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
305 310 315 320

Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
325 330

<210> 71
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Bromealin signal sequence

<400> 71
atggcctgga aggtgcaggt ggtgttcctc ttcctcttcc tctgcgtgat gtgggcctcc 60
ccgtccgcgc cctccgcc 78

<210> 72
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Bromealin signal peptide

<400> 72
Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala
20 25

<210> 73
<211> 1050
<212> DNA
<213> Artificial Sequence

<220>
<223> pSYN11000

<400> 73
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 ccgtccgcgc cctccgcgga cgagccgtcc gacccgatga tgaagcgctt cgaggagtgg 120
 atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgccg cttccagatc 180
 ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctccacacc 240
 ctccggcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc 300
 ggcatctccc gcccgctcaa catcgagcgc gagccggtgg tgtccttcga cgacgtggac 360
 atctccgcgc tgcgcagtc catcgactgg cgcgactacg gcgccgtgac ctccgtgaag 420
 aaccagaacc cgtgcggcgc ctgctgggccc ttccgcgcca tcgccaccgt ggagtccatc 480
 tacaagatca agaagggcac cctcgagccg ctctccgagc agcaggtgct cgactgcgcc 540
 aagggtctacg gctgcaaggg cggctgggag ttccgcgcct tcgagttcat catctccaac 600
 aagggcgtgg cctccggcgc catctacccg tacaaggccg ccaagggcac ctgcaagacc 660
 gacggcgtgc cgaactccgc ctacatcacc ggctacgccc gcgtgccgcg caacaacgag 720
 tcctccatga tgtacgccgt gtccaagcag ccgatcaccg tggccgtgga cgccaacgcc 780
 aacttccagt actacaagtc cggcgtgttc aacggcccgt gcggcacctc cctcaaccac 840
 gccgtgaccg ccacggcta cggccaggac tccatcatct acccgaagaa gtggggcgcc 900
 aagtggggcg aggcggcta catccgatg gcccgcgacg tgtcctctc ctccggcatc 960
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 gccgccaact ccaccctcgt ggccgagtag . 1050

<210> 74
 <211> 1067
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN11589

<400> 74
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 cgtccgcgc ctcgcctcc tcctctctct tcgccgactc caaccgatc cgcccggtga 120
 ccgaccgcgc cgctccacc gacgagccgt ccgaccgat gatgaagcgc ttcgaggagt 180
 ggatggtgga gtacggccgc gtgtacaagg acaacgacga gaagatgcgc cgcttccaga 240
 tcttcaagaa caacgtgaac cacatcgaga ccttcaactc ccgcaacgag aactcctaca 300
 cctcggcat caaccagttc accgacatga ccaacaacga gttcatcgcc cagtacaccg 360

gcggcatctc ccgcccgc acatcgagc gcgagccggt ggtgtccttc gacgacgtgg 420
 acatctccgc cgtgccgcag tccatcgact ggcgcgacta cggcgccgtg acctccgtga 480
 agaaccagaa cccgtgcggc gcctgctggg ccttcgccgc catcgccacc gtggagtcca 540
 tctacaagat caagaagggc atcctcgagc cgctctccga gcagcagggtg ctcgactgcg 600
 ccaagggtta cggctgcaag ggcggctggg agttccgcgc cttcgagttc atcatctcca 660
 acaaggcggt ggcttccggc gccatctacc cgtacaaggc cgccaagggc acctgcaaga 720
 ccgacggcgt gccgaactcc gcctacatca ccggctacgc ccgctgcccg cgcaacaacg 780
 agtctctcat gatgtacgcc gtgtccaagc agccgatcac cgtggccgtg gacgccaacg 840
 ccaacttcca gtaactacaag tccggcgtgt tcaacggccc gtgcggcacc tccctcaacc 900
 acgcccgtgac cgccatcggc tacggccagg actccatcat ctacccgaag aagtggggcg 960
 ccaagtgggg cgaggccggc tacatccgca tggcccgcga cgtgtcctcc tctccggca 1020
 tctgcggcat cgccatcgac ccgctctacc cgaccctcga ggagtag 1067

<210> 75
 <211> 1023
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN11587 Sequence

<400> 75
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 ccgtccgcgc cctccgcgga cgagccgtcc gaccgatga tgaagcgctt cgaggagtgg 120
 atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgcgc cttccagatc 180
 ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctctacacc 240
 ctggcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc 300
 ggcatctccc gcccgctcaa catcgagcgc gagccggtgg tgtccttcga cgacgtggac 360
 atctccgcgc tggcgagtc catcgactgg cgcgactacg gcgcccgtgac ctccgtgaag 420
 aaccagaacc cgtgcggcgc ctgctgggccc ttccgcgcca tcgccaccgt ggagtccatc 480
 tacaagatca agaaggcat cctcgagccg ctctccgagc agcagggtgct cgactgcgcc 540
 aagggtacg gctgcaaggc cggctgggag ttccgcgcct tcgagttcat catctccaac 600
 aagggcgtgg cctccggcgc catctacccg tacaaggccg ccaagggcac ctgcaagacc 660
 gacggcgtgc cgaactccgc ctacatcacc ggctacgccc gcgtgccgcg caacaacgag 720

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tcttccatga tgtacgccgt gtccaagcag ccgatcaccg tggccgtgga cgccaacgcc 780
aacttccagt actacaagtc cggcgtgttc aacggcccgt gcggcacctc cctcaaccac 840
gccgtgaccg ccatcggcta cggccaggac tccatcatct acccgaagaa gtggggcgcc 900
aagtggggcg aggcgggcta catccgcagt gcccgcgacg tgtcctcttc ctccggcatc 960
tgcggcatcg ccatcgaccc gctctacccg accctcgagg agtccgagaa ggacgagctg 1020
tag 1023

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<210> 76
<211> 990
<212> DNA
<213> Artificial Sequence

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<220>
<223> pSYN12169 Sequence

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```

<400> 76
atgagggtgt tgcctcgttg cctcgtcttc ctggctctcg ctgcgagcgc cacctccatg 60
gcggacgagc cgtccgaccc gatgatgaag cgcttcgagg agtggatggt ggagtacggc 120
cgcgtgraca aggacaacga cgagaagatg cggcgcttcc agatcttcaa gaacaacgtg 180
aaccacatcg agaccttcaa ctcccgcac gagaaactct acaccctcgg catcaaccag 240
ttcaccgaca tgaccaacaa cgagttcatc gcccagtaca ccggcggcac ctcccgcctg 300
ctcaacatcg agcgcgagcc ggtggtgtcc ttcgacgacg tggacatctc cgccgtgccg 360
cagtcacatg actggcgaga ctacggcgcc gtgacctcgg tgaagaacca gaaccctgac 420
ggcgccctgt gggccttcgc cgccatcgcc accgtggagt ccatctacaa gatcaagaag 480
ggcctcctcg agccgctctc cgagcagcag gtgctcgact gcgccaaggg ctacggctgc 540
aaggcgccgt gggagttccg cgccttcgag ttcatcatct ccaacaaggg cgtggcctcc 600
ggcgccatct acccgtaaaa ggccgccaag ggcacctgca agaccgacgg cgtgccgaac 660
tcgccttaca tcaccggcta cggccgcgtg ccgcgcaaca acgagtcctc catgatgtac 720
gccgtgtcca agcagccgat caccgtggcc gtggacgcca acgccaactt ccagtactac 780
aagtccggcg tgttcaacgg cccgtgcggc acctccctca accacgccgt gaccgccatc 840
ggctacggcc aggaactccat catctacccg aagaagtggg gcgccaagtg gggcgaggcc 900
ggctacatcc gcatggcccg cgacgtgtcc tcctcctcgg gcatctgcgg catcgccatc 960
gaccgcctct acccgacctt cgaggagtag 990

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<210> 77
 <211> 1170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN12575 Sequence

<400> 77
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 gacgcgtcca cgttcgcgcc cggcgcgcgc cagggcctga ggggggcccg ggcgtcggcg 120
 gcggcgagaca cgctcagcat gcggaccagc gcgcgcgcgc cgcccaggca ccagcaccag 180
 cagggcgccc gcggggccag gttcccgtcg ctcgtcgtgt gcgccagcgc cggcgccatg 240
 gcggacgagc cgtccgacct gatgatgaag cgcttcgagg agtggatggt ggagtacggc 300
 cgcgtgtaca aggacaacga cgagaagatg cgccgcttcc agatcttcaa gaacaacgtg 360
 aaccacatcg agaccttcaa ctcccgcaac gagaactcct acaccctcgg catcaaccag 420
 ttccacgaca tgaccaacaa cgagttcatc gcccagtaca ccggcggcat ctcccgcccg 480
 ctcaacatcg agcgcgagcc ggtggtgtcc ttcgacgacg tggacatctc cgccgtgccg 540
 cagtccatcg actggcgcca ctacggcgcc gtgacctccg tgaagaacca gaaccctgac 600
 ggcgcctgct gggccttcgc cgccatcgcc accgtggagt ccatctacaa gatcaagaag 660
 ggcatacctc agccgctctc cgagcagcag gtgctcgact gcgccaaggg ctacggctgc 720
 aagggcggtt gggagttccg cgccttcgag ttcatcatct ccaacaaggg cgtggcctcc 780
 ggcgccatct acccgtaaaa ggccgccaag ggcacctgca agaccgacgg cgtgccgaac 840
 tccgcctaca tcaccggcra cgcccgcgtg ccgcgcaaca acgagtcctc catgatgtac 900
 gccgtgtcca agcagccgat caccgtggcc gtggacgcca acgccaactt ccagtactac 960
 aagtcgcggc tgttcaacgg ccgctgcggc acctccctca accacgccgt gaccgccatc 1020
 ggctacggcc aggaactccat catctacccg aagaagtggg gcgccaagtg gggcgaggcc 1080
 ggctacatcc gcatggcccc cgacgtgtcc tctcctccg gcatctgcgg catcgccatc 1140
 gaccgcctct acccgaccct cgaggagtag 1170

<210> 78
 <211> 1068
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSM270 Sequence

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<400> 78
atggcctgga aggtgcaggt ggtgttcttc ttctctttcc tctgcgtgat gtgggcctcc 60
ccgtccgcgc cctccgcctc ctctctctcc ttccgcgact ccaacccgat ccgcccggtg 120
accgaccgcg ccgcctccac cgacgagccg tccgaccgga tgatgaagcg cttcgaggag 180
tggatggtgg agtacggccg cgtgtacaag gacaacgacg agaagatgcg ccgcttccag 240
atcttcaaga acaacgtgaa ccacatcgag accttcaact cccgcaacga gaactcctac 300
accctcggca tcaaccagtt caccgacatg accaacaacg agttcatcgc ccagtacacc 360
ggcggcatct cccgcccgtt caacatcgag cgcgagccgg tgggtgtcctt cgacgacgtg 420
gacatctccg ccgtgccgca gtccatcgac tggcgcgact acggcgccgt gacctccgtg 480
aagaaccaga acccgtgcgg cgcttgctgg gccttcgccg ccacgcccac cgtggagtcc 540
atctacaaga tcaagaaggg catcctcgag ccgctctccg agcagcaggt gctcgactgc 600
gccaaggggt acggctgcaa gggcggtgg gagttccgcg ccttcgagtt catcatctcc 660
aacaagggcg tggcctccgg cgccatctac ccgtacaagg ccgccaaggg cacctgcaag 720
accgacggcg tgccgaactc cgcctacatc accggctacg cccgcgtgcc gcgcaacaac 780
gagtcctcca tgatgtacgc cgtgtccaag cagccgatca ccgtggccgt ggacgccaac 840
gccaacttcc agtactacaa gtccggcgtg ttcaacggcc cgtgcggcac ctccctcaac 900
cacgccgtga ccgccatcgg ctacggccag gactccatca tctacccgaa gaagtggggc 960
gccaagtggg gcgaggccgg ctacatccgc atggcccgcg acgtgtcctc ctctccgggc 1020
atctgcggca tcgccatcga ccgctctac ccgaccctcg aggagtag 1068

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<210> 79
<211> 1497
<212> DNA
<213> Trichoderma reesei

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<220>
<221> CDS
<222> (1)..(1497)
<223> Trichoderma reesei cellobiohydrolase I

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<400> 79
atg cag tcg gcg tgt act ctc caa tcg gag act cac ccg cct ctg aca 48
Met Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
1 5 10 15

tgg cag aaa tgc tcg tct ggt ggc acg tgc act caa cag aca ggc tcc 96
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
20 25 30

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gtg gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac agc agc Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser 35 40 45	144
acg aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt cct gac Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp 50 55 60	192
aac gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc tac gcg Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala 65 70 75 80	240
tcc acg tac gga gtt acc acg agc ggt aac agc ctc tcc att ggc ttt Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe 85 90 95	288
gtc acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac ctt atg Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met 100 105 110	336
gcg agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac gag ttc Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe 115 120 125	384
tct ttc gat gtt gat gtt tcg cag ctg ccg tgc ggc ttg aac gga gct Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala 130 135 140	432
ctc tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag tat ccc Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro 145 150 155 160	480
acc aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac agc cag Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln 165 170 175	528
tgt ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt gag ggc Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly 180 185 190	576
tgg gag ccg tca tcc aac aac gcg aac acg ggc att gga gga cac gga Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly 195 200 205	624
agc tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc tcc gag Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu 210 215 220	672
gct ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc tgc gag Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu 225 230 235 240	720
ggt gat ggg tgc ggc gga act tac tcc gat aac aga tat ggc ggc act Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr 245 250 255	768
tgc gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc aac acc Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr	816

260							265							270							
agc	ttc	tac	ggc	cct	ggc	tct	agc	ttt	acc	ctc	gat	acc	acc	aag	aaa						864
Ser	Phe	Tyr	Gly	Pro	Gly	Ser	Ser	Phe	Thr	Leu	Asp	Thr	Thr	Lys	Lys						
		275						280					285								
ttg	acc	gtt	gtc	acc	cag	ttc	gag	acg	tcg	ggc	gcc	atc	aac	cga	tac						912
Leu	Thr	Val	Val	Thr	Gln	Phe	Glu	Thr	Ser	Gly	Ala	Ile	Asn	Arg	Tyr						
	290					295					300										
tat	gtc	cag	aat	ggc	gtc	act	ttc	cag	cag	ccc	aac	gcc	gag	ctt	ggc						960
Tyr	Val	Gln	Asn	Gly	Val	Thr	Phe	Gln	Gln	Pro	Asn	Ala	Glu	Leu	Gly						
305					310					315					320						
agt	tac	tct	ggc	aac	gag	ctc	aac	gat	gat	tac	tgc	aca	gct	gag	gag						1008
Ser	Tyr	Ser	Gly	Asn	Glu	Leu	Asn	Asp	Asp	Tyr	Cys	Thr	Ala	Glu	Glu						
				325					330					335							
gca	gaa	ttc	ggc	gga	tcc	tct	ttc	tca	gac	aag	ggc	ggc	ctg	act	cag						1056
Ala	Glu	Phe	Gly	Gly	Ser	Ser	Phe	Ser	Asp	Lys	Gly	Gly	Leu	Thr	Gln						
			340					345					350								
ttc	aag	aag	gct	acc	tct	ggc	ggc	atg	gtt	ctg	gtc	atg	agt	ctg	tgg						1104
Phe	Lys	Lys	Ala	Thr	Ser	Gly	Gly	Met	Val	Leu	Val	Met	Ser	Leu	Trp						
		355				360						365									
gat	gat	tac	tac	gcc	aac	atg	ctg	tgg	ctg	gac	tcc	acc	tac	ccg	aca						1152
Asp	Asp	Tyr	Tyr	Ala	Asn	Met	Leu	Trp	Leu	Asp	Ser	Thr	Tyr	Pro	Thr						
	370					375					380										
aac	gag	acc	tcc	tcc	aca	ccc	ggc	gcc	gtg	cgc	gga	agc	tgc	tcc	acc						1200
Asn	Glu	Thr	Ser	Ser	Thr	Pro	Gly	Ala	Val	Arg	Gly	Ser	Cys	Ser	Thr						
385					390					395					400						
agc	tcc	ggc	gtc	cct	gct	cag	gtc	gaa	tct	cag	tct	ccc	aac	gcc	aag						1248
Ser	Ser	Gly	Val	Pro	Ala	Gln	Val	Glu	Ser	Gln	Ser	Pro	Asn	Ala	Lys						
				405				410						415							
gtc	acc	ttc	tcc	aac	atc	aag	ttc	gga	ccc	att	ggc	agc	acc	ggc	aac						1296
Val	Thr	Phe	Ser	Asn	Ile	Lys	Phe	Gly	Pro	Ile	Gly	Ser	Thr	Gly	Asn						
			420					425					430								
cct	agc	ggc	ggc	aac	cct	ccc	ggc	gga	aac	ccg	cct	ggc	acc	acc	acc						1344
Pro	Ser	Gly	Gly	Asn	Pro	Pro	Gly	Gly	Asn	Pro	Pro	Gly	Thr	Thr	Thr						
		435					440					445									
acc	cgc	cgc	cca	gcc	act	acc	act	gga	agc	tct	ccc	gga	cct	acc	cag						1392
Thr	Arg	Arg	Pro	Ala	Thr	Thr	Thr	Gly	Ser	Ser	Pro	Gly	Pro	Thr	Gln						
	450					455					460										
tct	cac	tac	ggc	cag	tgc	ggc	ggc	att	ggc	tac	agc	ggc	ccc	acg	gtc						1440
Ser	His	Tyr	Gly	Gln	Cys	Gly	Gly	Ile	Gly	Tyr	Ser	Gly	Pro	Thr	Val						
465					470					475					480						
tgc	gcc	agc	ggc	aca	act	tgc	cag	gtc	ctg	aac	cct	tac	tac	tct	cag						1488
Cys	Ala	Ser	Gly	Thr	Thr	Cys	Gln	Val	Leu	Asn	Pro	Tyr	Tyr	Ser	Gln						
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tgc ctg taa
Cys Leu

1497

<210> 80
<211> 498
<212> FRT
<213> Trichoderma reesei

<400> 80

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35 40 45

Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
50 55 60

Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
65 70 75 80

Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
85 90 95

Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
100 105 110

Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
115 120 125

Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
130 135 140

Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
145 150 155 160

Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
165 170 175

Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
180 185 190

Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
 195 200 205

Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
 210 215 220

Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
 225 230 235 240

Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
 245 250 255

Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
 260 265 270

Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
 275 280 285

Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
 290 295 300

Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
 305 310 315 320

Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
 325 330 335

Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
 340 345 350

Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
 355 360 365

Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
 370 375 380

Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
 385 390 395 400

Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
 405 410 415

Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
420 425 430

Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
435 440 445

Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
450 455 460

Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
465 470 475 480

Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
485 490 495

Cys Leu

<210> 31
<211> 1365
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1365)
<223> trichoderma reesei cellobiohydrolase II

<400> 81
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tct ggt ggc cag aat tgg tgg ggt ccg act tgc tgt gct tcc gga agc 96
Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser
20 25 30
aca tgc gtc tac tcc aac gac tat tac tcc cag tgt ctt ccc ggc gct 144
Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala
35 40 45
gca agc tca agc tcg tcc acg cgc gcc gcg tcg acg act tca cga gta 192
Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val
50 55 60
tcc ccc aca aca tcc cgg tcg agc tcc gcg acg cct cca cct ggt tct 240
Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser
65 70 75 80
acc act acc aga gta cct cca gtc gga tcg gga acc gct acg tat tca 288
Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser

85								90				95				
ggc aac cct ttt gtt ggg gtc act cct tgg gcc aat gca tat tac gcc	Gly Asn Pro Phe 100	Val Gly Val Thr Pro 105	Trp Ala Asn Ala Tyr 110	Tyr Ala	336											
tct gaa gtt agc agc ctc gct att cct agc ttg act gga gcc atg gcc	Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala	115	120	125	384											
act gct gca gca gct gtc gca aag gtt ccc tct ttt atg tgg cta gat	Thr Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp	130	135	140	432											
act ctt gac aag acc cct ctc atg gag caa acc ttg gcc gac atc cgc	Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg	145	150	155	480											
acc gcc aac aag aat ggc ggt aac tat gcc gga cag ttt gtg gtg tat	Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr	165	170	175	528											
gac ttg ccg gat cgc gat tgc gct gcc ctt gcc tcg aat ggc gaa tac	Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr	180	185	190	576											
tct att gcc gat ggt ggc gtc gcc aaa tat aag aac tat atc gac acc	Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr	195	200	205	624											
att cgt caa att gtc gtg gaa tat tcc gat atc cgg acc ctc ctg gtt	Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val	210	215	220	672											
att gag cct gac tct ctt gcc aac ctg gtg acc aac ctc ggt act cca	Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro	225	230	235	720											
aag tgt gcc aat gct cag tca gcc tac ctt gag tgc atc aac tac gcc	Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala	245	250	255	768											
gtc aca cag ctg aac ctt cca aat gtt gcg atg tat ttg gac gct ggc	Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly	260	265	270	816											
cat gca gga tgg ctt ggc tgg ccg gca aac caa gac ccg gcc gct cag	His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln	275	280	285	864											
cta ttt gca aat gtt tac aag aat gca tcg tct ccg aga gct ctt cgc	Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg	290	295	300	912											
gga ttg gca acc aat gtc gcc aac tac aac ggg tgg aac att acc agc	Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser	305	310	315	960											

ccc cca tcg tac acg caa ggc aac gct gtc tac aac gag aag ctg tac 1008
 Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr
 325 330 335
 atc cac gct att gga cct ctt ctt gcc aat cac ggc tgg tcc aac gcc 1056
 Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala
 340 345 350
 ttc ttc atc act gat caa ggt cga tcg gga aag cag cct acc gga cag 1104
 Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln
 355 360 365
 caa cag tgg gga gac tgg tgc aat gtg atc ggc acc gga ttt ggt att 1152
 Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile
 370 375 380
 cgc cca tcc gca aac act ggg gac tcg ttg ctg gat tcg ttt gtc tgg 1200
 Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp
 385 390 395 400
 gtc aag cca ggc ggc gag tgt gac ggc acc agc gac agc agt gcg cca 1248
 Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro
 405 410 415
 cga ttt gac tcc cac tgt gcg ctc cca gat gcc ttg caa ccg gcg cct 1296
 Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro
 420 425 430
 caa gct ggt gct tgg ttc caa gcc tac ttt gtg cag ctt ctc aca aac 1344
 Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn
 435 440 445
 gca aac cca tcg ttc ctg tag 1365
 Ala Asn Pro Ser Phe Leu
 450

<210> 52
 <211> 454
 <212> PRT
 <213> Trichoderma reesei

<400> 82

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 Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser
 20 25 30
 Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala
 35 40 45
 Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val
 50 55 60

Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser
 65 70 75 80

Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser
 85 90 95

Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala
 100 105 110

Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala
 115 120 125

Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp
 130 135 140

Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg
 145 150 155 160

Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr
 165 170 175

Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr
 180 185 190

Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr
 195 200 205

Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val
 210 215 220

Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro
 225 230 235 240

Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala
 245 250 255

Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly
 260 265 270

His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln
 275 280 285

Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg
290 295 300

Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser
305 310 315 320

Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr
325 330 335

Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala
340 345 350

Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln
355 360 365

Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile
370 375 380

Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp
385 390 395 400

Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro
405 410 415

Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro
420 425 430

Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn
435 440 445

Ala Asn Pro Ser Phe Leu
450

<210> 83
<211> 1317
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1317)
<223> Trichoderma reesei endoglucanase I

<400> 83
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Met Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr

48

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gtg gtc ctt gac tgg aac tac cgc tgg atg cac gac gca aac tac aac Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn 35 40 45				144
tcg tgc acc gtc aac ggc ggc gtc aac acc acg ctc tgc cct gac gag Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu 50 55 60				192
gcg acc tgt ggc aag aac tgc ttc atc gag ggc gtc gac tac gcc gcc Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala 65 70 75 80				240
tcg ggc gtc acg acc tcg ggc agc agc ctc acc atg aac cag tac atg Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met 85 90 95				288
ccc agc agc tct ggc ggc tac agc agc gtc tct cct cgg ctg tat ctc Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu 100 105 110				336
ctg gac tct gac ggt gag tac gtg atg ctg aag ctc aac ggc cag gag Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu 115 120 125				384
ctg agc ttc gac gtc gac ctc tct gct ctg ccg tgt gga gag aac ggc Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly 130 135 140				432
tcg ctc tac ctg tct cag atg gac gag aac ggg ggc gcc aac cag tat Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr 145 150 155 160				480
aac acg gcc ggt gcc aac tac ggg agc ggc tac tgc gat gct cag tgc Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys 165 170 175				528
ccc gtc cag aca tgg agg aac ggc acc ctc aac act agc cac cag ggc Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly 180 185 190				576
ttc tgc tgc aac gag atg gat atc ctg gag ggc aac tcg agg gcg aat Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn 195 200 205				624
gcc ttg acc cct cac tct tgc acg gcc acg gcc tgc gac tct gcc ggt Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly 210 215 220				672
tgc ggc ttc aac ccc tat ggc agc ggc tac aaa agc tac tac ggc ccc Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro 225 230 235 240				720

gga gat acc gtt gac acc tcc aag acc ttc acc atc atc acc cag ttc Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe 245 250 255	768
aac acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc acc cgc Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg 260 265 270	816
aag tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc ggc ggc Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly 275 280 285	864
gac acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc ctc gcc Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala 290 295 300	912
acc atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc agc att Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile 305 310 315 320	960
tgg aac gac aac agc cag tac atg aac tgg ctc gac agc ggc aac gcc Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala 325 330 335	1008
ggc ccc tgc agc agc acc gag ggc aac cca tcc aac acc ctg gcc aac Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn 340 345 350	1056
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ggg tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg tcc agc Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser 370 375 380	1152
acg acg ttt tcg act aca cgg agg agc tcg acg act tcg agc agc ccg Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro 385 390 395 400	1200
agc tgc acg cag act cac tgg ggg cag tgc ggt ggc att ggg tac agc Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser 405 410 415	1248
ggg tgc aag acg tgc acg tcg ggc act acg tgc cag tat agc aac gac Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp 420 425 430	1296
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<210> 84
 <211> 438
 <212> PRT
 <213> Trichoderma reesei

<400> 84

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          20          25          30

Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
          35          40          45

Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
50          55          60

Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
65          70          75          80

Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
          85          90          95

Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu
          100          105          110

Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
          115          120          125

Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly
130          135          140

Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
145          150          155          160

Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
          165          170          175

Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
          180          185          190

Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
          195          200          205

Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
210          215          220

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Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
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Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
245 250 255

Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
260 265 270

Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
275 280 285

Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
290 295 300

Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
305 310 315 320

Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
325 330 335

Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn
340 345 350

Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
355 360 365

Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
370 375 380

Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
385 390 395 400

Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
405 410 415

Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
420 425 430

Tyr Tyr Ser Gln Cys Leu
435

<210> 85
<211> 954

<212> DNA
 <213> Artificial Sequence

<220>
 <223> 6GP1

<220>
 <221> CDS
 <222> (1)..(954)
 <223> 6GP1

<400> 85
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aac atc ggc aac gcc ctg gag gcc ccg aac gag ggc gac tgg ggc gtg 96
 Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val
 20 25 30

gtg atc aag gac gag ttc ttc gac atc atc aag gag gcc ggc ttc tcc 144
 Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser
 35 40 45

cac gtg cgc atc ccg atc cgc tgg tcc acc cac gcc tac gcc ttc ccg 192
 His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro
 50 55 60

ccg tac aag atc atg gac cgc ttc ttc aag cgc gtg gac gag gtg atc 240
 Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile
 65 70 75 80

aac ggc gcc ctc aag cgc ggc ctc gcc gtg gcc atc aac atc cac cac 288
 Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His
 85 90 95

tac gag gag ctc atg aac gac ccg gag gag cac aag gag cgc ttc ctc 336
 Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu
 100 105 110

gcc ctc tgg aag cag atc gcc gac cgc tac aag gac tac ccg gag acc 384
 Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr
 115 120 125

ctc ttc ttc gag atc ctc aac gag ccg cac ggc aac ctc acc ccg gag 432
 Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu
 130 135 140

aag tgg aac gag ctg ctc gag gag gcc ctc aag gtg atc cgc tcc atc 480
 Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile
 145 150 155 160

gac aag aag cac acc atc atc att ggc acc gca gag tgg gga ggc atc 528
 Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile
 165 170 175

tcc gcc ctc gag aag ctc tcc gtg ccg aag tgg gag aag aat tcc atc 576

Ser	Ala	Leu	Glu	Lys	Leu	Ser	Val	Pro	Lys	Trp	Glu	Lys	Asn	Ser	Ile		
			180					185					190				
gtg	acc	atc	cac	tac	tac	aac	ccg	ttc	gag	ttc	acg	cac	cag	ggc	gcc		624
Val	Thr	Ile	His	Tyr	Tyr	Asn	Pro	Phe	Glu	Phe	Thr	His	Gln	Gly	Ala		
		195					200					205					
gag	tgg	gtg	gag	ggc	tcc	gag	aag	tgg	ctt	ggc	cgc	aag	tgg	ggc	tcc		672
Glu	Trp	Val	Glu	Gly	Ser	Glu	Lys	Trp	Leu	Gly	Arg	Lys	Trp	Gly	Ser		
	210					215				220							
ccg	gac	gac	cag	aag	cac	ctc	atc	gag	gag	ttc	aac	ttc	atc	gag	gag		720
Pro	Asp	Asp	Gln	Lys	His	Leu	Ile	Glu	Glu	Phe	Asn	Phe	Ile	Glu	Glu		
225					230					235					240		
tgg	tcc	aag	aag	aac	aag	cgc	ccg	atc	tac	atc	ggc	gag	ttt	ggc	gcc		768
Trp	Ser	Lys	Lys	Asn	Lys	Arg	Pro	Ile	Tyr	Ile	Gly	Glu	Phe	Gly	Ala		
				245					250					255			
tac	cgc	aag	gcc	gac	ctc	gag	tcc	cgc	atc	aag	tgg	acc	tcc	ttc	gtg		816
Tyr	Arg	Lys	Ala	Asp	Leu	Glu	Ser	Arg	Ile	Lys	Trp	Thr	Ser	Phe	Val		
			260					265					270				
gtg	cgt	gag	atg	gag	aag	cgc	cgc	tgg	tcc	tgg	gcc	tac	tgg	gag	ttc		864
Val	Arg	Glu	Met	Glu	Lys	Arg	Arg	Trp	Ser	Trp	Ala	Tyr	Trp	Glu	Phe		
		275				280						285					
tgc	tcc	ggc	ttc	ggc	gtg	tac	gac	acc	ctc	cgc	aag	acc	tgg	aac	aag		912
Cys	Ser	Gly	Phe	Gly	Val	Tyr	Asp	Thr	Leu	Arg	Lys	Thr	Trp	Asn	Lys		
	290					295					300						
gac	ctc	ctc	gag	gcc	ctc	atc	ggc	ggc	gac	tcc	atc	gag	tag				954
Asp	Leu	Leu	Glu	Ala	Leu	Ile	Gly	Gly	Asp	Ser	Ile	Glu					
305					310					315							

<210> 86
 <211> 317
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 86

Met	Gly	Val	Asp	Pro	Phe	Glu	Arg	Asn	Lys	Ile	Leu	Gly	Arg	Gly	Ile		
1				5					10					15			

Asn	Ile	Gly	Asn	Ala	Leu	Glu	Ala	Pro	Asn	Glu	Gly	Asp	Trp	Gly	Val		
		20						25					30				

Val	Ile	Lys	Asp	Glu	Phe	Phe	Asp	Ile	Ile	Lys	Glu	Ala	Gly	Phe	Ser		
		35					40					45					

His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro
 50 55 60

Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile
 65 70 75 80

Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His
 85 90 95

Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu
 100 105 110

Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr
 115 120 125

Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu
 130 135 140

Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile
 145 150 155 160

Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile
 165 170 175

Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile
 180 185 190

Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala
 195 200 205

Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser
 210 215 220

Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu
 225 230 235 240

Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala
 245 250 255

Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val
 260 265 270

Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe
 275 280 285

Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys
 290 295 300

Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu
 305 310 315

<210> 87
 <211> 1248
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(1248)
 <223> Barley AmyI amylase

<400> 87
 atg gca cac caa gtc ctc ttt cag ggg ttc aac tgg gag tcg tgg aag 48
 Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
 1 5 10 15
 cag agc ggc ggg tgg tac aac atg atg atg ggc aag gtc gac gac atc 96
 Gln Ser Gly Gly Trp Tyr Asn Met Met Met Gly Lys Val Asp Asp Ile
 20 25 30
 gcc gct gcc gga gtc acc cac gtc tgg ctg cca ccg ccg tcg cac tcc 144
 Ala Ala Ala Gly Val Thr His Val Trp Leu Pro Pro Pro Ser His Ser
 35 40 45
 gtc tcc aac gaa ggt tac atg cct ggt cgg ctg tac gac atc gac gcg 192
 Val Ser Asn Glu Gly Tyr Met Pro Gly Arg Leu Tyr Asp Ile Asp Ala
 50 55 60
 tcc aag tac ggc aac gcg gcg gag ctc aag tcg ctc atc ggc gcg ctc 240
 Ser Lys Tyr Gly Asn Ala Ala Glu Leu Lys Ser Leu Ile Gly Ala Leu
 65 70 75 80
 cac ggc aag ggc gtg cag gcc atc gcc gac atc gtc atc aac cac cgc 288
 His Gly Lys Gly Val Gln Ala Ile Ala Asp Ile Val Ile Asn His Arg
 85 90 95
 tgc gcc gac tac aag gat agc cgc ggc atc tac tgc atc ttc gag ggc 336
 Cys Ala Asp Tyr Lys Asp Ser Arg Gly Ile Tyr Cys Ile Phe Glu Gly
 100 105 110
 ggc acc tcc gac ggc cgc ctc gac tgg ggc ccc cac atg atc tgt cgc 384
 Gly Thr Ser Asp Gly Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg
 115 120 125
 gac gac acc aaa tac tcc gat ggc acc gca aac ctc gac acc gga gcc 432
 Asp Asp Thr Lys Tyr Ser Asp Gly Thr Ala Asn Leu Asp Thr Gly Ala
 130 135 140

gac ttc gcc gcc gcg ccc gac atc gac cac ctc aac gac cgg gtc cag Asp Phe Ala Ala Ala Pro Asp Ile Asp His Leu Asn Asp Arg Val Gln 145 150 155 160	480
cgc gag ctc aag gag tgg ctc ctc tgg ctc aag agc gac ctc ggc ttc Arg Glu Leu Lys Glu Trp Leu Leu Trp Leu Lys Ser Asp Leu Gly Phe 165 170 175	528
gac gcg tgg cgc ctt gac ttc gcc agg ggc tac tcg ccg gag atg gcc Asp Ala Trp Arg Leu Asp Phe Ala Arg Gly Tyr Ser Pro Glu Met Ala 180 185 190	576
aag gtg tac atc gac ggc aca tcc ccg agc ctc gcc gtg gcc gag gtg Lys Val Tyr Ile Asp Gly Thr Ser Pro Ser Leu Ala Val Ala Glu Val 195 200 205	624
tgg gac aat atg gcc acc ggc ggc gac ggc aag ccc aac tac gac cag Trp Asp Asn Met Ala Thr Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln 210 215 220	672
gac gcg cac cgg cag aat ctg gtg aac tgg gtg gac aag gtg ggc ggc Asp Ala His Arg Gln Asn Leu Val Asn Trp Val Asp Lys Val Gly Gly 225 230 235 240	720
gcg gcc tcg gca ggc atg gtg ttc gac ttc acg acc aaa ggg ata ctg Ala Ala Ser Ala Gly Met Val Phe Asp Phe Thr Thr Lys Gly Ile Leu 245 250 255	768
aac gct gcc gtg gag ggc gag ctg tgg agg ctg atc gac ccg cag ggg Asn Ala Ala Val Glu Gly Glu Leu Trp Arg Leu Ile Asp Pro Gln Gly 260 265 270	816
aag gcc ccc ggc gtg atg gga tgg tgg ccg gcc aag gcc gtc acc ttc Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe 275 280 285	864
gtc gac aac cac gat aca ggc tcc acg cag gcc atg tgg cca ttc ccc Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro 290 295 300	912
tcc gac aag gtc atg cag ggc tac gcg tac atc ctc acc cac ccc ggc Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly 305 310 315 320	960
atc cca tgc atc ttc tac gac cat ttc ttc aac tgg ggg ttt aag gac Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp 325 330 335	1008
cag atc gcg gcg ctg gtg gcg atc agg aag cgc aac ggc atc acg gcg Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala 340 345 350	1056
acg agc gct ctg aag atc ctc atg cac gaa gga gat gcc tac gtc gcc Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala 355 360 365	1104
gag ata gac ggc aag gtg gtg gtg aag atc ggg tcc agg tac gac gtc Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val 1152	

370 375 380
 ggg gcg gtg atc ccg gcc ggg ttc gtg acc tcg gca cac ggc aac gac 1200
 Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp
 385 390 395 400
 tac gcc gtc tgg gag aag aac ggt gcc gcg gca aca cta caa cgg agc 1248
 Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Ala Thr Leu Gln Arg Ser
 405 410 415

 <210> 88
 <211> 416
 <212> PRT
 <213> Hordeum vulgare

 <400> 88
 Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
 1 5 10 15
 Gln Ser Gly Gly Trp Tyr Asn Met Met Met Gly Lys Val Asp Asp Ile
 20 25 30
 Ala Ala Ala Gly Val Thr His Val Trp Leu Pro Pro Pro Ser His Ser
 35 40 45
 Val Ser Asn Glu Gly Tyr Met Pro Gly Arg Leu Tyr Asp Ile Asp Ala
 50 55 60
 Ser Lys Tyr Gly Asn Ala Ala Glu Leu Lys Ser Leu Ile Gly Ala Leu
 65 70 75 80
 His Gly Lys Gly Val Gln Ala Ile Ala Asp Ile Val Ile Asn His Arg
 85 90 95
 Cys Ala Asp Tyr Lys Asp Ser Arg Gly Ile Tyr Cys Ile Phe Glu Gly
 100 105 110
 Gly Thr Ser Asp Gly Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg
 115 120 125
 Asp Asp Thr Lys Tyr Ser Asp Gly Thr Ala Asn Leu Asp Thr Gly Ala
 130 135 140
 Asp Phe Ala Ala Ala Pro Asp Ile Asp His Leu Asn Asp Arg Val Gln
 145 150 155 160

Arg Glu Leu Lys Glu Trp Leu Leu Trp Leu Lys Ser Asp Leu Gly Phe
 165 170 175

Asp Ala Trp Arg Leu Asp Phe Ala Arg Gly Tyr Ser Pro Glu Met Ala
 180 185 190

Lys Val Tyr Ile Asp Gly Thr Ser Pro Ser Leu Ala Val Ala Glu Val
 195 200 205

Trp Asp Asn Met Ala Thr Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln
 210 215 220

Asp Ala His Arg Gln Asn Leu Val Asn Trp Val Asp Lys Val Gly Gly
 225 230 235 240

Ala Ala Ser Ala Gly Met Val Phe Asp Phe Thr Thr Lys Gly Ile Leu
 245 250 255

Asn Ala Ala Val Glu Gly Glu Leu Trp Arg Leu Ile Asp Pro Gln Gly
 260 265 270

Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe
 275 280 285

Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro
 290 295 300

Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly
 305 310 315 320

Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp
 325 330 335

Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala
 340 345 350

Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala
 355 360 365

Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val
 370 375 380

Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp
 385 390 395 400

Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Ala Thr Leu Gln Arg Ser
 405 410 415

<210> 89
 <211> 1401
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Trichoderma reesei β -Glucosidase 2

<220>
 <221> CDS
 <222> (1)..(1401)
 <223> Trichoderma reesei β -Glucosidase 2

<400> 89
 atg ttg ccc aag gac ttt cag tgg ggg ttc gcc acg gct gcc tac cag 48
 Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
 1 5 10 15
 atc gag ggc gcc gtc gac cag gac ggc cgc ggc ccc agc atc tgg gac 96
 Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
 20 25 30
 acg ttc tgc gcg cag ccc ggc aag atc gcc gac ggc tcg tcg ggc gtg 144
 Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
 35 40 45
 acg gcg tgc gac tcg tac aac cgc acg gcc gag gac att gcg ctg ctg 192
 Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
 50 55 60
 aag tcg ctc ggg gcc aag agc tac cgc ttc tcc atc tcg tgg tcg cgc 240
 Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
 65 70 75 80
 atc atc ccc gag ggc ggc cgc ggc gat gcc gtc aac cag gcg ggc atc 288
 Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
 85 90 95
 gac cac tac gtc aag ttc gtc gac gac ctg ctc gac gcc ggc atc acg 336
 Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
 100 105 110
 ccc ttc atc acc ctc ttc cac tgg gac ctg ccc gag ggc ctg cat cag 384
 Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
 115 120 125
 cgg tac ggg ggg ctg ctg aac cgc acc gag ttc ccg ctc gac ttt gaa 432
 Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
 130 135 140
 aac tac gcc cgc gtc atg ttc agg gcg ctg ccc aag gtg cgc aac tgg 480

Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp 145 150 155 160	
atc acc ttc aac gag ccg ctg tgc tcg gcc atc ccg ggc tac ggc tcc Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser 165 170 175	528
ggc acc ttc gcc ccc ggc cgg cag agc acc tcg gag ccg tgg acc gtc Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val 180 185 190	576
ggc cac aac atc ctc gtc gcc cac ggc cgc gcc gtc aag gcg tac cgc Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg 195 200 205	624
gac gac ttc aag ccc gcc agc ggc gac ggc cag atc ggc atc gtc ctc Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu 210 215 220	672
aac ggc gac ttc acc tac ccc tgg gac gcc gcc gac ccg gcc gac aag Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys 225 230 235 240	720
gag gcg gcc gag cgg cgc ctc gag ttc ttc acg gcc tgg ttc gcg gac Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp 245 250 255	768
ccc atc tac ttg ggc gac tac ccg gcg tcg atg cgc aag cag ctg ggc Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly 260 265 270	816
gac cgg ctg ccg acc ttt acg ccc gag gag cgc gcc ctc gtc cac ggc Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly 275 280 285	864
tcc aac gac ttt tac ggc atg aac cac tac acg tcc aac tac atc cgc Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg 290 295 300	912
cac cgc agc tcg ccc gcc tcc gcc gac gac acc gtc ggc aac gtc gac His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp 305 310 315 320	960
gtg ctc ttc acc aac aag cag ggc aac tgc atc ggc ccc gag acg cag Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln 325 330 335	1008
tcc ccc tgg ctg cgc ccc tgt gcc gcc ggc ttc cgc gac ttc ctg gtg Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val 340 345 350	1056
tgg atc agc aag agg tac ggc tac ccg ccc atc tac gtg acg gag aac Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn 355 360 365	1104
ggc acg agc atc aag ggc gag agc gac ttg ccc aag gag aag att ctc Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu 370 375 380	1152

gaa gat gac ttc agg gtc aag tac tat aac gag tac atc cgt gcc atg 1200
 Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
 385 390 395 400
 gtt acc gcc gtg gag ctg gac ggg gtc aac gtc aag ggg tac ttt gcc 1248
 Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
 405 410 415
 tgg tcg ctc atg gac aac ttt gag tgg gcg gac ggc tac gtg acg agg 1296
 Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
 420 425 430
 ttt ggg gtt acg tat gtg gat tat gag aat ggg cag aag cgg ttc ccc 1344
 Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
 435 440 445
 aag aag agc gca aag agc ttg aag ccg ctg ttt gac gag ctg att gcg 1392
 Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
 450 455 460
 gcg gcg tga 1401
 Ala Ala
 465

<210> 90
 <211> 466
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 90

Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
 1 5 10 15
 Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
 20 25 30
 Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
 35 40 45
 Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
 50 55 60
 Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
 65 70 75 80
 Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
 85 90 95

Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
100 105 110

Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
115 120 125

Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
130 135 140

Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp
145 150 155 160

Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser
165 170 175

Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val
180 185 190

Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg
195 200 205

Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu
210 215 220

Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys
225 230 235 240

Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp
245 250 255

Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly
260 265 270

Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly
275 280 285

Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg
290 295 300

His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp
305 310 315 320

Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln
325 330 335

Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val
340 345 350

Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn
355 360 365

Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu
370 375 380

Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
385 390 395 400

Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
405 410 415

Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
420 425 430

Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
435 440 445

Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
450 455 460

Ala Ala
465

<210> 91
<211> 2103
<212> DNA
<213> Artificial Sequence

<220>
<223> Trichoderma reesei β -Glucosidase D

<220>
<221> CDS
<222> (1)..(2103)
<223> Trichoderma reesei β -Glucosidase D

<400> 91
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Met Ile Leu Gly Cys Glu Ser Thr Gly Val Ile Ser Ala Val Lys His
1 5 10 15

48

ttt gtc gcc aac gac cag gag cac gag cgg cga gcg gtc gac tgt ctc Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu 20 25 30	96
atc acc cag cgg gct ctc cgg gag gtc tat ctg cga ccc ttc cag atc Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile 35 40 45	144
gta gcc cga gat gca agg ccc ggc gca ttg atg aca tcc tac aac aag Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys 50 55 60	192
gtc aat ggc aag cac gtc gct gac agc gcc gag ttc ctt cag ggc att Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile 65 70 75 80	240
ctc cgg act gag tgg aat tgg gac cct ctc att gtc agc gac tgg tac Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr 85 90 95	288
ggc acc tac acc act att gat gcc atc aaa gcc ggc ctt gat ctc gag Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu 100 105 110	336
atg cgg gcc gtt tca cga tat cgc ggc aaa tac atc gag tct gct ctg Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu 115 120 125	384
cag gcc cgt ttg ctg aag cag tcc act atc gat gag cgc gct cgc cgc Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg 130 135 140	432
gtg ctc agg ttc gcc cag aag gcc agc cat ctc aag gtc tcc gag gta Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val 145 150 155 160	480
gag caa ggc cgt gac ttc cca gag gat cgc gtc ctc aac cgt cag atc Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile 165 170 175	528
tgc ggc agc agc att gtc cta ctg aag aat gag aac tcc atc tta cct Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro 180 185 190	576
ctc ccc aag tcc gtc aag aag gtc gcc ctt gtt ggt tcc cac gtg cgt Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg 195 200 205	624
cta ccg gct atc tcg gga gga ggc agc gcc tct ctt gtc cct tac tat Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr 210 215 220	672
gcc ata tct cta tac gat gcc gtc tct gag gta cta gcc ggt gcc acg Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr 225 230 235 240	720
atc acg cac gag gtc ggt gcc tat gcc cac caa atg ctg ccc gtc atc	768

Ile	Thr	His	Glu	Val	Gly	Ala	Tyr	Ala	His	Gln	Met	Leu	Pro	Val	Ile	
				245					250					255		
gac	gca	atg	atc	agc	aac	gcc	gta	atc	cac	ttc	tac	aac	gac	ccc	atc	816
Asp	Ala	Met	Ile	Ser	Asn	Ala	Val	Ile	His	Phe	Tyr	Asn	Asp	Pro	Ile	
			260					265					270			
gat	gtc	aaa	gac	aga	aag	ctc	ctt	ggc	agt	gag	aac	gta	tcg	tcg	aca	864
Asp	Val	Lys	Asp	Arg	Lys	Leu	Leu	Gly	Ser	Glu	Asn	Val	Ser	Ser	Thr	
		275					280					285				
tcg	ttc	cag	ctc	atg	gat	tac	aac	aac	atc	cca	acg	ctc	aac	aag	gcc	912
Ser	Phe	Gln	Leu	Met	Asp	Tyr	Asn	Asn	Ile	Pro	Thr	Leu	Asn	Lys	Ala	
	290					295				300						
atg	ttc	tgg	ggc	act	ctc	gtg	ggc	gag	ttt	atc	cct	acc	gcc	acg	gga	960
Met	Phe	Trp	Gly	Thr	Leu	Val	Gly	Glu	Phe	Ile	Pro	Thr	Ala	Thr	Gly	
305				310					315						320	
att	tgg	gaa	ttt	ggc	ctc	agt	gtc	ttt	ggc	act	gcc	gac	ctt	tat	att	1008
Ile	Trp	Glu	Phe	Gly	Leu	Ser	Val	Phe	Gly	Thr	Ala	Asp	Leu	Tyr	Ile	
			325					330					335			
gat	aat	gag	ctc	gtg	att	gaa	aat	aca	aca	cat	cag	acg	cgt	gga	acc	1056
Asp	Asn	Glu	Leu	Val	Ile	Glu	Asn	Thr	Thr	His	Gln	Thr	Arg	Gly	Thr	
			340					345					350			
gcc	ttt	ttc	gga	aag	gga	acg	acg	gaa	aaa	gtc	gct	acc	agg	agg	atg	1104
Ala	Phe	Phe	Gly	Lys	Gly	Thr	Thr	Glu	Lys	Val	Ala	Thr	Arg	Arg	Met	
		355					360					365				
gtg	gcc	ggc	agc	acc	tac	aag	ctg	cgt	ctc	gag	ttt	ggg	tct	gcc	aac	1152
Val	Ala	Gly	Ser	Thr	Tyr	Lys	Leu	Arg	Leu	Glu	Phe	Gly	Ser	Ala	Asn	
	370					375					380					
acg	acc	aag	atg	gag	acg	acc	ggc	gtt	gtc	aac	ttt	ggc	ggc	ggc	gcc	1200
Thr	Thr	Lys	Met	Glu	Thr	Thr	Gly	Val	Val	Asn	Phe	Gly	Gly	Gly	Ala	
385				390						395					400	
gta	cac	ctg	ggc	gcc	tgt	ctc	aag	gtc	gac	cca	cag	gag	atg	att	gcg	1248
Val	His	Leu	Gly	Ala	Cys	Leu	Lys	Val	Asp	Pro	Gln	Glu	Met	Ile	Ala	
			405					410					415			
cgg	gcc	gtc	aag	gcc	gca	gcc	gat	gcc	gac	tac	acc	atc	atc	tgc	acg	1296
Arg	Ala	Val	Lys	Ala	Ala	Ala	Asp	Ala	Asp	Tyr	Thr	Ile	Ile	Cys	Thr	
		420					425						430			
gga	ctc	agc	ggc	gag	tgg	gag	tct	gag	ggc	ttt	gac	cgg	cct	cac	atg	1344
Gly	Leu	Ser	Gly	Glu	Trp	Glu	Ser	Glu	Gly	Phe	Asp	Arg	Pro	His	Met	
		435					440					445				
gac	ctg	ccc	cct	ggc	gtg	gac	acc	atg	atc	tcg	caa	gtt	ctt	gac	gcc	1392
Asp	Leu	Pro	Pro	Gly	Val	Asp	Thr	Met	Ile	Ser	Gln	Val	Leu	Asp	Ala	
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gct	ccc	aat	gct	gta	gtc	gtc	aac	cag	tca	ggc	acc	cca	gtg	aca	atg	1440
Ala	Pro	Asn	Ala	Val	Val	Val	Asn	Gln	Ser	Gly	Thr	Pro	Val	Thr	Met	
465				470						475					480	

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Ser	Trp	Ala	His	Lys	Ala	Lys	Ala	Ile	Val	Gln	Ala	Trp	Tyr	Gly	Gly	
				485					490					495		
aac	gag	aca	ggc	cac	gga	atc	tcc	gat	gtg	ctc	ttt	ggc	aac	gtc	aac	1536
Asn	Glu	Thr	Gly	His	Gly	Ile	Ser	Asp	Val	Leu	Phe	Gly	Asn	Val	Asn	
			500					505					510			
ccg	tcg	ggg	aaa	ctc	tcc	cta	tcg	tgg	cca	gtc	gat	gtg	aag	cac	aac	1584
Pro	Ser	Gly	Lys	Leu	Ser	Leu	Ser	Trp	Pro	Val	Asp	Val	Lys	His	Asn	
		515					520					525				
cca	gca	tat	ctc	aac	tac	gcc	agc	gtt	ggt	gga	cgg	gtc	ttg	tat	ggc	1632
Pro	Ala	Tyr	Leu	Asn	Tyr	Ala	Ser	Val	Gly	Gly	Arg	Val	Leu	Tyr	Gly	
	530					535					540					
gag	gat	gtt	tac	gtt	ggc	tac	aag	ttc	tac	gac	aaa	acg	gag	agg	gag	1680
Glu	Asp	Val	Tyr	Val	Gly	Tyr	Lys	Phe	Tyr	Asp	Lys	Thr	Glu	Arg	Glu	
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Val	Leu	Phe	Pro	Phe	Gly	His	Gly	Leu	Ser	Tyr	Ala	Thr	Phe	Lys	Leu	
				565				570						575		
cca	gat	tct	acc	gtg	agg	acg	gtc	ccc	gaa	acc	ttc	cac	ccg	gac	cag	1776
Pro	Asp	Ser	Thr	Val	Arg	Thr	Val	Pro	Glu	Thr	Phe	His	Pro	Asp	Gln	
			580					585					590			
ccc	aca	gta	gcc	att	gtc	aag	atc	aag	aac	acg	agc	agt	gtc	ccg	ggc	1824
Pro	Thr	Val	Ala	Ile	Val	Lys	Ile	Lys	Asn	Thr	Ser	Ser	Val	Pro	Gly	
		595					600					605				
gcc	cag	gtc	ctg	cag	tta	tac	att	tcg	gcc	cca	aac	tcg	cct	aca	cat	1872
Ala	Gln	Val	Leu	Gln	Leu	Tyr	Ile	Ser	Ala	Pro	Asn	Ser	Pro	Thr	His	
	610					615					620					
cgc	ccg	gtc	aag	gag	ctg	cac	gga	ttc	gaa	aag	gtg	tat	ctt	gaa	gct	1920
Arg	Pro	Val	Lys	Glu	Leu	His	Gly	Phe	Glu	Lys	Val	Tyr	Leu	Glu	Ala	
625					630					635					640	
ggc	gag	gag	aag	gag	gta	caa	ata	ccc	att	gac	cag	tac	gct	act	agc	1968
Gly	Glu	Glu	Lys	Glu	Val	Gln	Ile	Pro	Ile	Asp	Gln	Tyr	Ala	Thr	Ser	
				645				650						655		
ttc	tgg	gac	gag	att	gag	agc	atg	tgg	aag	agc	gag	agg	ggc	att	tat	2016
Phe	Trp	Asp	Glu	Ile	Glu	Ser	Met	Trp	Lys	Ser	Glu	Arg	Gly	Ile	Tyr	
			660					665					670			
gat	gtg	ctt	gta	gga	ttc	tcg	agt	cag	gaa	atc	tcg	ggc	aag	ggg	aag	2064
Asp	Val	Leu	Val	Gly	Phe	Ser	Ser	Gln	Glu	Ile	Ser	Gly	Lys	Gly	Lys	
		675					680					685				
ctg	att	gtg	cct	gaa	acg	cga	ttc	tgg	atg	ggg	ctg	tag				2103
Leu	Ile	Val	Pro	Glu	Thr	Arg	Phe	Trp	Met	Gly	Leu					
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<210> 92
 <211> 700
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 92

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Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
 20 25 30

Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile
 35 40 45

Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys
 50 55 60

Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile
 65 70 75 80

Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr
 85 90 95

Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu
 100 105 110

Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu
 115 120 125

Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg
 130 135 140

Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val
 145 150 155 160

Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile
 165 170 175

Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro
 180 185 190

Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg
 195 200 205

Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr
 210 215 220

Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr
 225 230 235 240

Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile
 245 250 255

Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile
 260 265 270

Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr
 275 280 285

Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala
 290 295 300

Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
 305 310 315 320

Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
 325 330 335

Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr
 340 345 350

Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
 355 360 365

Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
 370 375 380

Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
 385 390 395 400

Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
 405 410 415

Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
 420 425 430

Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
 435 440 445

Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
 450 455 460

Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
 465 470 475 480

Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
 485 490 495

Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
 500 505 510

Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
 515 520 525

Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
 530 535 540

Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
 545 550 555 560

Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
 565 570 575

Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
 580 585 590

Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
 595 600 605

Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
 610 615 620

Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
 625 630 635 640

Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
 645 650 655

Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly-Ile Tyr
 660 665 670

Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
 675 680 685

Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
 690 695 700

<210> 93
 <211> 1496
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized CBHI

<400> 93
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 ggacccacgc caccaactcc tccaccaact gctacgacgg caacacctgg tcctccaccc 180
 tctgcccgga caacgagacc tgcgccaaga actgctgcct cgacggcgcc gcctacgcct 240
 ccacctacgg cgtgaccacc tccggcaact ccctctccat cggcttcgtg acccagtcgg 300
 cccagaagaa cgtgggcgcc cgctcttacc tcatggcctc cgacaccacc taccaggagt 360
 tcacccctct cggcaacgag ttctccttcg acgtggacgt gtcccagctc ccgtgcggcc 420
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 ccaacaccgc cggcgccaag tacggcaccg gctactgcga ctcccagtgc ccgcgcgacc 540
 tcaagttcat caacggccag gccaaacgtg agggctggga gccgtcctcc aacaacgcca 600
 acaccggcat cggcggccac ggctcctgct gctccgagat ggacatctgg gaggccaaact 660
 ccctctccga ggccctcacc ccgcacccgt gcaccaccgt gggccaggag atctgcgagg 720
 gcgacggctg cggcggcacc tactccgaca accgctacgg cggcacctgc gacccggacg 780
 gctgcgactg gaacccttac cgctcggca acacctcctt ctacggcccc ggctcctcct 840
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 gcccgaccca gtcccactac ggccagtgcg gcggcatcgg ctactccggc ccgaccgtgt 1440
 gcgcctccgg caccacctgc cagggtgtca acccgtaacta ctcccagtgc ctctag 1496

<210> 94
 <211> 1365
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized CBHII

<400> 94
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 aactggctcg gcccgacctg ctgcgcctcc ggctccacct gcgtgtactc caacgactac 120
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 aagtacaaga actacatcga caccatccgc cagatcgtgg tggagtactc cgacatccgc 660
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cactgggccc tcccggacgc cctccagccg gccccgcagg ccggcgcttg gttccaggcc 1320
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<210> 95
<211> 1317
<212> DNA
<213> Artificial Sequence

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<220>
<223> Maize optimized EGLI

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ccggcctcct ccaccacctt ctccaccacc cgccgctcct ccaccacctc ctctccccg 1200
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<210> 96
 <211> 1401
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized BGLII

<400> 96
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<210> 97
 <211> 2103
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized CEL3D

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 tccaacgccc tgatecactt ctacaacgac ccgatcgacg tgaaggaccg caagctcctc 840
 ggctccgaga acgtgtcctc cactccttc cagctcatgg actacaacaa catcccgacc 900
 ctcaacaagg ccatgttctg gggcaccctc gtgggcgagt tcatcccgac cgccaccggc 960
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 gagaagggtg ccaccgccc catggtggcc ggctccacct acaagctccg cctcgagttc 1140
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 gtgcacctcg gcgcctgcct caaggtggac ccgcaggaga tgatcgcccg cgccgtgaag 1260

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aagaacacct cctccgtgcc gggcgcccag gtgctccagc tctacatctc cggcccgaac 1860
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ggcgaggaga aggaggtgca gatcccgatc gaccagtacg ccacctcctt ctgggacgag 1980
atcgagtcca tgtggaagtc cgagcgcggc atctacgacg tgctcgtggg cttctctctc 2040
caggagatct ccggcaaggg caagctcatc gtgccggaga ccgcttctg gatgggcctc 2100
tag 2103

<210> 98
<211> 420
<212> DNA
<213> Zea mays

<220>
<223> Q protein promoter

<400> 98
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ctagttgtca caagttglat atcgattcgt cgcgtttcaa caactcatgc aacattacaa 120
acaagtaaca caatattaca aagttagttt catacaaagc aagaaaagga caataatact 180
tgacatgtaa agtgaagctt attatacttc ctaatccaac acaaaacaaa aaaaagttgc 240
acaaagggtc aaaaatccac atcaaccatt aacctatacg taaagtgagt gatgagtcac 300
atratccaac aaatgtttat caatgtggta tcatacaagc attgacatcc cataaatgca 360
agaaattgtg ccaacaaagc tataagtaac cctcatatgt atttgactc atgcatcaca 420

<210> 99
<211> 1188

<212> DNA

<213> artificial sequence

<220>

<223> synthetic ferulic acid esterase

<400> 99

atggccgcct cctccccgac catgccgccg tccggctacg accaggtgcg caacggcgtg	60
ccgcgcggcc aggtggtgaa catctcctac ttctccaccg ccaccaactc caccgcgccg	120
gcccgcgtgt acctccccgc gggctactcc aaggacaaga agtactccgt gctctacctc	180
ctccacggca tcggcggctc cgagaacgac tggttcgagg gcggcggccg cgccaacgtg	240
atcgccgaca acctcatcgc cgagggcaag atcaagccgc tcatcatcgt gaccccgaac	300
accaacgccg ccggccccgg catcgccgac ggctacgaga acttcaccaa ggacctctc	360
aactccctca tcccgtacat cgagtccaac tactccgtgt acaccgaccg cgagcaccgc	420
gccatcgccg gcctctctat gggcggcggc cagtccttca acatcggcct caccaacctc	480
gacaagttcg cctacatcgg cccgatctcc gccgccccga acacctaccg gaacgagcgc	540
ctcttccccg acggcggcaa ggccgccgcg gagaagctca agctcctctt catcgctgc	600
ggcaccaacg actccctcat cggcttcggc cagcgcgtgc acgagtactg cgtggccaac	660
aacatcaacc acgtgtactg gctcatccag ggcggcggcc acgacttcaa cgtgtggaag	720
ccggggcctct ggaacttctt ccagatggcc gacgaggccg gcctcaccgc cgacggcaac	780
accccggtgc cgaccccgtc cccgaagccg gccaacaccc gcatcgaggc cgaggactac	840
gacggcatca actcctctct catcgagatc atcggcgtgc cgccggaggg cggccgcggc	900
atcggctaca tcacctccgg cgactacctc gtgtacaagt ccatcgactt cggcaacggc	960
gccacctctt tcaaggccaa ggtggccaac gccaacacct ccaacatcga gcttcgcctc	1020
aacggccccg acggcaccct catcggcacc ctctccgtga agtccaccgg cgactggaac	1080
acctacgagg agcagacctg ctccatctcc aaggtgaccg gcatcaacga cctctacctc	1140
gtgttcaagg gcccggtgaa catcgactgg ttcaccttcg gcgtgtag	1188

<210> 100

<211> 395

<212> PRT

<213> artificial sequence

<220>

<223> synthetic ferulic acid esterase

<400> 100

Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val
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 Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
 20 25 30
 Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly
 35 40 45
 Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
 50 55 60
 Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
 65 70 75 80
 Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
 85 90 95
 Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
 100 105 110
 Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
 115 120 125
 Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
 130 135 140
 Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
 145 150 155 160
 Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
 165 170 175
 Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
 180 185 190
 Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
 195 200 205
 Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
 210 215 220
 Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
 225 230 235 240

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
275 280 285

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
385 390 395

<210> 101
<211> 1188
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13036

<400> 101
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ccgcgcggcc aggtggtgaa catctctac ttctccaccg ccaccaactc caccgcgccg 120
gcccgcgtgt acctcccgcc gggctactcc aaggacaaga agtactccgt gctctacctc 180
ctccacggca tcggcggtc cgagaacgac tggttcgagg gcggcggccg cgccaacgtg 240

atcgccgaca acctcatcgc cgagggcaag atcaagccgc tcatcatcgt gaccccgaac 300
 accaacgccc cgggcccggg catcgccgac ggctacgaga acttcaccaa ggacctctc 360
 aactccctca tcccgtacat cgagtcacaac tactccgtgt acaccgaccg cgagcaccgc 420
 gccatcgccg gcctctctat gggcgggcggc cagtccttca acatcggcct caccaacctc 480
 gacaagtctg cctacatcgg ccgcatctcc gccgccccga acacctaccg gaacgagcgc 540
 ctcttcccgg acggcgggcaa ggccgcccgc gagaagctca agtcctctt catcgcttgc 600
 ggcaccaacg actccctcat cggcttcggc cagcgcgtgc acgagtactg cgtggccaac 660
 aacatcaacc acgtgtactg gctcatccag ggcggcgggc acgacttcaa cgtgtggaag 720
 ccgggctctt ggaacttctt ccagatggcc gacgaggccg gcctcaccg cgacggcaac 780
 accccgggtg cgaccccgtc cccgaagccg gccaacaccc gcatcgaggc cgaggactac 840
 gacggcatca actcctctc catcgagatc atcggcgtgc cgccggaggg cggccgcggc 900
 atcggctaca tcacctcgg cgactacctc gtgtacaagt ccatcgactt cggcaacggc 960
 gccacctctt tcaaggccaa ggtggccaac gccaacacct ccaacatcga gcttcgcctc 1020
 aacggcccga acggcacctt catcggcacc ctctccgtga agtcaccgg cgactggaac 1080
 acctacgagg agcagacctg ctccatctcc aaggtgaccg gcatcaacga cctctacctc 1140
 gtgttcaagg gcccggtgaa catcgactgg ttacacctc gcggtgtag 1188

<210> 102
 <211> 395
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13036

<400> 102

Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val
 1 5 10 15

Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
 20 25 30

Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly
 35 40 45

Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
 50 55 60

Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
 65 70 75 80
 Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
 85 90 95
 Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
 100 105 110
 Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
 115 120 125
 Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
 130 135 140
 Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
 145 150 155 160
 Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
 165 170 175
 Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
 180 185 190
 Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
 195 200 205
 Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
 210 215 220
 Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
 225 230 235 240
 Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
 245 250 255
 Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
 260 265 270
 Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
 275 280 285

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
385 390 395

<210> 103
<211> 1245
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13038

<400> 103
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gccgcctccc tcccgaacct gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120
cgcggccagg tgggtgaacat ctctacttc tccaccgcca ccaactccac ccgcccggcc 180
cgcgtgtacc tcccgcgggg ctactccaag gacaagaagt actccgtgct ctacctctc 240
cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300
gccgacaacc tcctcgcga gggcaagatc aagccgctca tcctcgtgac cccgaacacc 360
aacgcgcgcg gcccgggcat cgcgcgacgc tacgagaact tcaccaagga cctcctcaac 420
tcctcctcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 480
atcgcgcggc tctctatggg cggcggccag tctttcaaca tcggcctcac caacctcgac 540
aagttcgctt acatcggccc gatctcggcc gccccgaaca cctacccgaa cgagcgcctc 600
ttcccggacg gcggcaaggc cgcgcgcgag aagctcaagc tcctcttcat cgctgcggc 660

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accaacgact ccctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac 720
atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 780
ggcctctgga acttctcca gatggccgac gagggccggc tcacccgcga cggcaacacc 840
ccggtgccga ccccgteccc gaagccggcc aacacccgca tcgaggccga ggactacgac 900
ggcatcaact cctctccat cgagatcatc ggcgtgccgc cggagggcgg ccgcggcatc 960
ggctacatca cctcggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc 1020
acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1080
ggcccgaacg gcacctcat cggcacctc tccgtgaagt ccaccggcga ctggaacacc 1140
tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg 1200
ttcaagggcc cggtgaacat cgactggttc accttcggcg tgtag 1245

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<210> 104
<211> 414
<212> PRT
<213> artificial sequence

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<220>
<223> plasmid 13038 aa

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<400> 104

```

```

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1          5          10          15

```

```

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20          25          30

```

```

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35          40          45

```

```

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50          55          60

```

```

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65          70          75          80

```

```

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
85          90          95

```

```

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
100          105          110

```

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
115 120 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
130 135 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
145 150 155 160

Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
165 170 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
180 185 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
195 200 205

Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
210 215 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
225 230 235 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
245 250 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
260 265 270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
275 280 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
 340 345 350

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
 355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
 370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
 385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
 405 410

<210> 105
 <211> 1425
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 13039

<400> 105
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 gacgcgtcca cgttcgcgcg cggcgccgcg cagggcctga ggggggcccg ggcgtcggcg 120
 gcggcggaca cgctcagcat gcggaccagc gcgcgcgcgg cgcccaggca ccagcaccag 180
 caggcgcgcc gcggggccag gttcccgtcg ctcgctcgtgt gcgccagcgc cggcgccatg 240
 gccgcctccc tcccgaacct gccgcgcgtc ggctacgacc aggtgcgcaa cggcgtgccg 300
 cgcggccagg tgggtgaacat ctctacttcc tccaccgcca ccaactccac ccgcccggcc 360
 cgcgtgtacc tcccgcgggg ctactccaag gacaagaagt actccgtgct ctacctctc 420
 cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 480
 gccgacaacc tcatcgccga gggcaagatc aagccgctca tcatcgtgac cccgaacacc 540
 aacgcgcgcg gcccgggcat cgccgacggc tacgagaact tcaccaagga cctcctcaac 600
 tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 660
 atcgccggcc tctctatggg cggcgggcag tccttcaaca tcggcctcac caacctcgac 720
 aagttcgctt acatcgggcc gatctccgcc gccccgaaca cctaccgaa cgagcgctc 780
 ttcccggacg gcggcaaggc cgccgcgcag aagctcaagc tcctcttcat cgcctgcggc 840
 accaacgact ccctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac 900

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atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg      960
ggcctcttga acttcctcca gatggccgac gagggccggc tcacccgcga cggcaacacc      1020
ccgggtgcga ccccgctccc gaagccggcc aacacccgca tcgaggccga ggactacgac      1080
ggcatcaact cctcctccat cgagatcatc ggcgtgccgc cggagggcgg ccgcggcatc      1140
ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc      1200
acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac      1260
ggcccgaacg gcacctcat cggcaccctc tccgtgaagt ccaccggcga ctggaaacacc      1320
tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg      1380
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```

<210> 106
 <211> 474
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13039 aa

<400> 106

```

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1           5           10          15

```

```

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
20          25          30

```

```

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
35          40          45

```

```

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
50          55          60

```

```

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
65          70          75          80

```

```

Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val Arg
85          90          95

```

```

Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser Thr
100         105         110

```

Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly Tyr
 115 120 125

Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile Gly
 130 135 140

Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val Ile
 145 150 155 160

Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile Val
 165 170 175

Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr Glu
 180 185 190

Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu Ser
 195 200 205

Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly Leu
 210 215 220

Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu Asp
 225 230 235 240

Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr Pro
 245 250 255

Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys Leu
 260 265 270

Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly Phe
 275 280 285

Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His Val
 290 295 300

Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys Pro
 305 310 315 320

Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr Arg
 325 330 335

Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn Thr
 340 345 350

Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile Glu
355 360 365

Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile Thr
370 375 380

Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly Ala
385 390 395 400

Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile Glu
405 410 415

Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser Val
420 425 430

Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser Ile
435 440 445

Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly Pro
450 455 460

Val Asn Ile Asp Trp Phe Thr Phe Gly Val
465 470

<210> 107
<211> 1263
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13347

<400> 107
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gccgcctccc tcccgaccat gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120
cgcggccagg tggagaacat ctctacttc tccaccgcca ccaactccac ccgcccggcc 180
cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctctc 240
cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300
gccgacaacc tcacgcccga gggcaagatc aagccgctca tcacgtgac cccgaacacc 360
aacgccgccg gcccgggcat cgcgcacggc tacgagaact tcaccaagga cctcctcaac 420
tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 480

atcgccggcc tctctatggg cggcggccag tccttcaaca tcggcctcac caacctcgac 540
aagttcgctt acatcgggcc gatctccgcc gccccgaaca cctaccgaa cgagcgctc 600
ttcccggacg gcggcaaggc cggccgcgag aagctcaagc tcctcttcat cgcctgcggc 660
accaacgact cctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac 720
atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 780
ggcctctgga acttctcca gatggccgac gaggccggcc tcaccgcga cggcaacacc 840
ccggtgccga cccgctccc gaagccggcc aacaccgca tcgaggccga ggactacgac 900
ggcatcaact cctctccat cgagatcatc ggcgtgccgc cggaggcg cgcggcatc 960
ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc 1020
acctcttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgctcaac 1080
ggccgaacg gcacctcat cggcaccctc tccgtgaagt ccaccggcga ctggaacacc 1140
tacgaggagc agacctgct catctccaag gtgaccggca tcaacgacct ctacctcgtg 1200
ttcaagggcc cgggtgaacat cgactggttc accttcggcg tgtccgagaa ggacgaactc 1260
tag 1263

<210> 108
<211> 420
<212> PRT
<213> artificial sequence

<220>
<223> plasmid 13347

<400> 108

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20 25 30

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35 40 45

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50 55 60

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65 70 75 80

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
 85 90 95
 Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
 100 105 110
 Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
 115 120 125
 Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
 130 135 140
 Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
 145 150 155 160
 Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
 165 170 175
 Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
 180 185 190
 Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
 195 200 205
 Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
 210 215 220
 Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
 225 230 235 240
 Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
 245 250 255
 Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
 260 265 270
 Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
 275 280 285
 Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
 290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
340 345 350

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val Ser Glu
405 410 415

Lys Asp Glu Leu
420

<210> 109
<211> 1296
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 11267

<400> 109
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gcgcagtcgc agccggagct gaagctggag tccgtggtga tcgtgtcccg ccacggcgctg 120
cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccggaacg ctggccgacc 180
tggccggtga agctcggcga gctgaccccg cgcgggcgcg agctgatcgc ctacctcggc 240
cactactggc gccagcgctt cgtggccgac ggctcctcc cgaagtgcgg ctgcccgcag 300
tccggccagg tggccatcat cgccgacgtg gacgagcgca cccgcaagac cggcgaggcc 360
tctcgccgcg gcctcgcccc ggactgcgcc atcaccgtgc acaccaggc cgacacctcc 420
tccccggacc cgctcttcaa cccgctcaag accggcggtg gccagctcga caacgccaac 480
gtgaccgacg ccctcctgga gcgcgcccgc ggctccatcg ccgacttcac cggccactac 540

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cagaccgcct tccgcgagct ggagcgcggtg ctcaacttcc cgcagtcctaa cctctgcctc 600
aagcgcgaga agcaggacga gtcctgctcc ctcacccagg ccctcccgtc cgagctgaag 660
gtgtccgccc actgcgtgtc cctcaccggc gcggtgtccc tcgcctccat gctcaccgaa 720
atcttctctc tccagcaggc ccagggcctg ccggagccgg gctggggccc catcaccgac 780
tcccaccagt ggaacacct cctctccctc cacaacgccc agttcgacct cctccagcgc 840
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accccgccacc cgcgcagaa gcaggcctac ggcgtgaccc tcccgcctc cgtgctcttc 960
atgcgcggcc acgacaccaa cctcgccaac ctgcggcgcg ccctggagct gaactggacc 1020
ctcccgggcc agccggacaa caccgcgcg ggcggcgagc tgggtgttca gcgctggcgc 1080
cgctctctcg acaactccca gtggattcag gtgtccctcg tgttccagac cctccagcag 1140
atgcgcgaca agaccccgct ctccctcaac acccgccgg gcgaggtgaa gctcaccctc 1200
gccggtgctg aggagcgcaa cgcaccgggc atgtgtctcc tcgccggctt caccagatc 1260
gtgaacgagg ccgcctccc ggctgctcc ctctaa 1296

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<210> 110
<211> 431
<212> PRT
<213> artificial sequence

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<220>
<223> plasmid 11267 aa sequence

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<400> 110

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1           5           10          15

```

```

Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
20          25          30

```

```

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
35          40          45

```

```

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
50          55          60

```

```

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
65          70          75          80

```

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
 85 90 95

Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
 100 105 110

Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
 115 120 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
 130 135 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
 145 150 155 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
 165 170 175

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
 180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
 195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
 210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
 225 230 235 240

Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
 245 250 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
 260 265 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
 275 280 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
 290 295 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
 305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
405 410 415

Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
420 425 430

<210> 111
<211> 1314
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 11268

<400> 111
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cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccgagcgc ctggccgacc 180
tgcccggtga agctcggcga gctgaccccg cgcggcgggc agctgatcgc ctacctcggc 240
cactactggc gccagcgctt cgtggccgac ggcctcctcc cgaagtgcgg ctgcccgcag 300
tccggccagg tggccatcat cgcgcagctg gacgagcgca cccgcaagac cggcgaggcc 360
ttcgcgcgcg gcctcgcgcc ggactgcgcc atcaccgtgc acaccagggc cgacacctcc 420
tccccggacc cgctcttcaa cccgctcaag accggcggtg gccagctcga caacgccaac 480
gtgaccgacg ccattctgga gcgcgccggc ggctccatcg ccgacttcac cggccactac 540
cagaccgcct tccgcgagct ggagcgcgtg ctcaacttcc cgcagtcgaa cctctgcctc 600

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aagcgcgaga agcaggacga gtcctgctcc ctcacccagg ccctcccgtc cgagctgaag    660
gtgtccgczg actgcgtgtc cctcaccggc gccgtgtccc tcgcctccat gctcaccgaa    720
atcttctctc tccagcaggc ccagggcattg ccggagccgg gctggggccg catcaccgac    780
tcccaccagt ggaacaccct cctctccctc cacaacgccc agttcgacct cctccagcgc    840
accccggagg tggcccgctc ccgcgccacc ccgctcctcg acctcatcaa gaccgccctc    900
accccgcacc cgcgcagaa gcaggcctac ggcgtgaccc tcccgcctc cgtgctcttc    960
atgcgcggcc acgacaccaa cctcgccaac ctgcggcggc ccctggagct gaactggacc   1020
ctcccgggcc agccggacaa caccgcgccg ggcggcgagc tgggtgttcga gcgctggcgc   1080
cgctctctcg acaactccca gtggattcag gtgtccctcg tgttccagac cctccagcag   1140
atgcgcgaca agaccccgct ctccctcaac acccgcgccg gcgaggtgaa gctcaccctc   1200
gccggctgcg aggagcgcaa cgcgcagggc atgtgctccc tcgccggctt caccagatc   1260
gtgaacgagg cccgcctccc ggctgctcc ctctccgaga aggacgagct gtaa           1314

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<210> 112

<211> 437

<212> PRT

<213> artificial sequence

<220>

<223> plasmid 11268 amino acid sequence

<400> 112

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1           5           10           15

```

```

Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
20           25           30

```

```

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
35           40           45

```

```

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
50           55           60

```

```

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
65           70           75           80

```

```

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
85           90           95

```


Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
100 105 110

Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
115 120 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
130 135 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
145 150 155 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
165 170 175

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
225 230 235 240

Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
245 250 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
260 265 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
275 280 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
290 295 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
405 410 415

Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu Ser
420 425 430

Glu Lys Asp Glu Leu
435